

Aren0054.ST25.txt  
SEQUENCE LISTING

<110> Behan, Dominic P.  
Lehmann-B Bruinsma, Karin  
Chalmers, Derek T.  
Lowitz, Kevin P.  
Lin, I-Lin  
Dang, Huong T.  
Chen, Ruoping  
Liaw, Chen W.

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20          25          30

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Pro Pro Phe Gln His Pro Asp Leu Ser Pro Leu Leu Arg Tyr Ser Phe
35          40          45

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Glu Thr Met Ala Pro Thr Gly Leu Ser Ser Leu Thr Val Asn Ser Thr
50          55          60

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Ala Val Pro Thr Thr Pro Ala Ala Phe Lys Ser Leu Asn Leu Pro Leu
65          70          75          80

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Gln Ile Thr Leu Ser Ala Ile Met Ile Phe Ile Leu Phe Val Ser Phe
85          90          95

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Leu Gly Asn Leu Val Val Cys Leu Met Val Tyr Gln Lys Ala Ala Met
100          105          110

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Arg Ser Ala Ile Asn Ile Leu Leu Ala Ser Leu Ala Phe Ala Asp Met
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Leu Leu Ala Val Leu Asn Met Pro Phe Ala Leu Val Thr Ile Leu Thr
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Phe Trp Leu Phe Val Ile Glu Gly Val Ala Ile Leu Leu Ile Ile Ser  
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Ile Asp Arg Phe Leu Ile Ile Val Gln Arg Gln Asp Lys Leu Asn Pro  
180 185 190

Tyr Arg Ala Lys Val Leu Ile Ala Val Ser Trp Ala Thr Ser Phe Cys  
195 200 205

Val Ala Phe Pro Leu Ala Val Gly Asn Pro Asp Leu Gln Ile Pro Ser  
210 215 220

Arg Ala Pro Gln Cys Val Phe Gly Tyr Thr Thr Asn Pro Gly Tyr Gln  
225 230 235 240

Ala Tyr Val Ile Leu Ile Ser Leu Ile Ser Phe Phe Ile Pro Phe Leu  
245 250 255

Val Ile Leu Tyr Ser Phe Met Gly Ile Leu Asn Thr Leu Arg His Asn  
260 265 270

Ala Leu Arg Ile His Ser Tyr Pro Glu Gly Ile Cys Leu Ser Gln Ala  
275 280 285

Ser Lys Leu Gly Leu Met Ser Leu Gln Arg Pro Phe Gln Met Ser Ile  
290 295 300

Asp Met Gly Phe Lys Thr Arg Ala Phe Thr Thr Ile Leu Ile Leu Phe  
305 310 315 320

Ala Val Phe Ile Val Cys Trp Ala Pro Phe Thr Thr Tyr Ser Leu Val  
325 330 335

Ala Thr Phe Ser Lys His Phe Tyr Tyr Gln His Asn Phe Phe Glu Ile  
340 345 350

Ser Thr Trp Leu Leu Trp Leu Cys Tyr Leu Lys Ser Ala Leu Asn Pro  
355 360 365

Leu Ile Tyr Tyr Trp Arg Ile Lys Lys Phe His Asp Ala Cys Leu Asp  
370 375 380

Met Met Pro Lys Ser Phe Lys Phe Leu Pro Gln Leu Pro Gly His Thr  
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Thr Val Val

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gcgctagccc tctgggtctt cctgcgcgcg ctgcgcgtgc actcgggtgtg gacggtgtac 180  
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 35 40 45  
 Arg Ala Leu Arg Val His Ser Val Val Ser Val Tyr Met Cys Asn Leu  
 50 55 60  
 Ala Ala Ser Asp Leu Leu Phe Thr Leu Ser Leu Pro Val Arg Leu Ser  
 65 70 75 80  
 Tyr Tyr Ala Leu His His Trp Pro Phe Pro Asp Leu Leu Cys Gln Thr  
 85 90 95  
 Thr Gly Ala Ile Phe Gln Met Asn Met Tyr Gly Ser Cys Ile Phe Leu  
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Val Trp Ala Leu Ile Leu Val Phe Ala Val Pro Ala Ala Arg Val His  
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Arg Pro Ser Arg Cys Arg Tyr Arg Asp Leu Glu Val Arg Leu Cys Phe  
165 170 175

Glu Ser Phe Ser Asp Glu Leu Trp Lys Gly Arg Leu Leu Pro Leu Val  
180 185 190

Leu Leu Ala Glu Ala Leu Gly Phe Leu Leu Pro Leu Ala Ala Val Val  
195 200 205

Tyr Ser Ser Gly Arg Val Phe Trp Thr Leu Ala Arg Pro Asp Ala Thr  
210 215 220

Gln Ser Gln Arg Arg Arg Lys Thr Val Arg Leu Leu Leu Ala Asn Leu  
225 230 235 240

Val Ile Phe Leu Leu Cys Phe Val Pro Tyr Asn Ser Thr Leu Ala Val  
245 250 255

Tyr Gly Leu Leu Arg Ser Lys Leu Val Ala Ala Ser Val Pro Ala Arg  
260 265 270

Asp Arg Val Arg Gly Val Leu Met Val Met Val Leu Leu Ala Gly Ala  
275 280 285

Asn Cys Val Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ala Glu Gly Phe  
290 295 300

Arg Asn Thr Leu Arg Gly Leu Gly Thr Pro His Arg Ala Arg Thr Ser  
305 310 315 320

Ala Thr Asn Gly Thr Arg Ala Ala Leu Ala Gln Ser Glu Arg Ser Ala  
325 330 335

Val Thr Thr Asp Ala Thr Arg Pro Asp Ala Ala Ser Gln Gly Leu Leu  
340 345 350

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Asp Ser Ala Leu  
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Gly Ala Leu Leu Val Val Val Leu Arg Thr Pro Gly Leu Arg Asp Ala
35          40          45
Leu Tyr Leu Ala His Leu Cys Val Val Asp Leu Leu Ala Ala Ala Ser
50          55          60
Ile Met Pro Leu Gly Leu Leu Ala Ala Pro Pro Pro Gly Leu Gly Arg
65          70          75          80
Val Arg Leu Gly Pro Ala Pro Cys Arg Ala Ala Arg Phe Leu Ser Ala
85          90          95
Ala Leu Leu Pro Ala Cys Thr Leu Gly Val Ala Ala Leu Gly Leu Ala
100         105         110
Arg Tyr Arg Leu Ile Val His Pro Leu Arg Pro Gly Ser Arg Pro Pro
115        120        125
Pro Val Leu Val Leu Thr Ala Val Trp Ala Ala Ala Gly Leu Leu Gly
130        135        140
Ala Leu Ser Leu Leu Gly Pro Pro Pro Ala Pro Pro Pro Ala Pro Ala
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Arg Cys Ser Val Leu Ala Gly Gly Leu Gly Pro Phe Arg Pro Leu Trp
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Gly Gly Ile Phe Val Val Ala Arg Arg Ala Ala Leu Arg Pro Pro Arg  
195 200 205

Pro Ala Arg Gly Ser Arg Leu Arg Ser Asp Ser Leu Asp Ser Arg Leu  
210 215 220

Ser Ile Leu Pro Pro Leu Arg Pro Arg Leu Pro Gly Gly Lys Ala Ala  
225 230 235 240

Leu Ala Pro Ala Leu Ala Val Gly Gln Phe Ala Ala Cys Trp Leu Pro  
245 250 255

Tyr Gly Cys Ala Cys Leu Ala Pro Ala Ala Arg Ala Ala Glu Ala Glu  
260 265 270

Ala Ala Val Thr Trp Val Ala Tyr Ser Ala Phe Ala Ala His Pro Phe  
275 280 285

Leu Tyr Gly Leu Leu Gln Arg Pro Val Arg Leu Ala Leu Gly Arg Leu  
290 295 300

Ser Arg Arg Ala Leu Pro Gly Pro Val Arg Ala Cys Thr Pro Gln Ala  
305 310 315 320

Trp His Pro Arg Ala Leu Leu Gln Cys Leu Gln Arg Pro Pro Glu Gly  
325 330 335

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20          25          30

Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala
35          40          45

Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp
50          55          60

Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu
65          70          75          80

Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val
85          90          95

Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg
100         105         110

Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly
115         120         125

Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro
130         135         140

Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val
145         150         155         160

Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro
165         170         175

Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala
180         185         190

Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met
195         200         205

Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu
210         215         220

Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro
225         230         235         240

Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu

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245

250

255

Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser  
 260 265 270

Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu  
 275 280 285

Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe  
 290 295 300

Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu  
 305 310 315 320

Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly  
 325 330 335

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&lt;211&gt; 1413

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 9

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20 25 30

Thr Val Phe Leu Val Ala Leu Leu Leu Gly Leu Pro Ala Asn Gly  
35 40 45

Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly Ala Gly Thr  
50 55 60

Arg Leu Ala Leu Leu Leu Ser Leu Ala Leu Ser Asp Phe Leu Phe  
65 70 75 80

Leu Ala Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His Gly Gly His  
85 90 95

Trp Pro Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe Leu Trp Gly  
100 105 110

Val Ser Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu Ser Leu Asp  
115 120 125

Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly His Arg Pro  
130 135 140

Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val Leu Ala Thr  
145 150 155 160

Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala Val Trp Trp  
165 170 175

Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu Glu Leu Ser  
180 185 190

Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe Leu Leu Leu  
195 200 205

Leu Val Cys His Val Leu Thr Gln Ala Thr Arg Thr Cys His Arg Gln  
210 215 220

Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg Val Ala Arg Thr Ile  
225 230 235 240

Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr Gln Leu Ala Gln Leu  
245 250 255

Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu Leu Trp  
260 265 270

## Aren0054.ST25.txt

Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser Cys Leu  
275 280 285

Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr Leu Leu  
290 295 300

Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu Arg Pro  
305 310 315 320

Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser Glu Gly  
325 330 335

Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met Asp Pro  
340 345 350

Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser Asp Pro  
355 360 365

Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser Asp Pro  
370 375 380

Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser Asp Ser  
385 390 395 400

Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln Thr Pro Ala Pro Ala  
405 410 415

Ala Ser Ser Val Pro Ser Pro Cys Asp Glu Ala Ser Pro Thr Pro Ser  
420 425 430

Ser His Pro Thr Pro Gly Ala Leu Glu Asp Pro Ala Thr Pro Pro Ala  
435 440 445

Ser Glu Gly Glu Ser Pro Ser Ser Thr Pro Pro Glu Ala Ala Pro Gly  
450 455 460

Ala Gly Pro Thr  
465

<210> 11  
<211> 1248  
<212> DNA  
<213> Homo sapiens

<400> 11  
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ccattccaga aacacctgaa cagcaccgag gagtatctgg ccttcctctg cggacctcgg 120  
cgcagccact tcttcctccc cgtgtctgtg gtgtatgtgc caatttttgt ggtgggggtc 180  
attggcaatg tcctggtgtg cctggtgatt ctgcagcacc aggctatgaa gacgcccacc 240  
aactactacc tcttcagcct ggcgggtctct gacctcctgg tcctgctcct tggaatgccc 300  
ctggagggtct atgagatgtg gcgcaactac cctttcttgt tcgggcccgt gggctgctac 360  
ttcaagacgg ccctctttga gaccgtgtgc ttgcctcca tcctcagcat caccaccgtc 420  
agcgtggagc gctacgtggc catcctacac ccgttcgcg ccaaactgca gagcaccggg 480  
cgccggggcc tcaggatcct cggcatcgtc tggggcttct ccgtgctctt ctccctgccc 540  
aacaccagca tccatggcat caagttccac tacttcccca atgggtccct ggtcccagg 600

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tcggccacct gtacggtcat caagcccatg tggatctaca atttcatcat ccaggtcacc 660
tccttcctat tctacctct ccccatgact gtcattcagt tcctctacta cctcatggca 720
ctcagactaa agaaagacaa atctcttgag gcagatgaag ggaatgcaaa tattcaaaga 780
ccctgcagaa aatcagtcaa caagatgctg tttgtcttg tcttagtggt tgctatctgt 840
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cagcggaaaca tcttcctgac agaatgccac tttgtggagc tgaccgaaga tataggtccc 1140
caattcccat gtcagtcata catgcacaac tctcacctcc caacagccct ctctagttaa 1200
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<210> 12
<211> 415
<212> PRT
<213> Homo sapiens

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<400> 12

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Met Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln
1          5          10          15
Lys Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr
20        25        30
Leu Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val
35        40        45
Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val
50        55        60
Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr
65        70        75        80
Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu
85        90        95
Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe
100       105       110
Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr
115       120       125
Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg
130       135       140
Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg
145       150       155       160
Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu
165       170       175
Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe
180       185       190

```

Aren0054.ST25.txt

Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys  
195 200 205

Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe  
210 215 220

Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala  
225 230 235 240

Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala  
245 250 255

Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val  
260 265 270

Leu Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg  
275 280 285

Leu Phe Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val  
290 295 300

Phe Asn Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser  
305 310 315 320

Ala Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala  
325 330 335

Ala Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln  
340 345 350

His Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu  
355 360 365

Cys His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys  
370 375 380

Gln Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu  
385 390 395 400

Gln Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr  
405 410 415

<210> 13  
<211> 1173  
<212> DNA  
<213> Homo sapiens

<400> 13  
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tttatgtcct tagtagcttt tgctataatg ctaggaaatg ctttggatcat tttagctttt 120  
gtggtggaca aaaaccttag acatcgaagt agttattttt ttcttaactt ggccatctct 180  
gacttctttg tgggtgtgat ctccattcct ttgtacatcc ctacacgct gttcgaatgg 240  
gattttggaa aggaaatctg tgtatttttg ctactactg actatctgtt atgtacagca 300  
tctgtatata acattgtcct catcagctat gatcgatacc tgtcagtctc aaatgctgtg 360  
tcttatagaa ctcaacatac tggggctctg aagattgtta ctctgatggg ggccggtttg 420  
gtgctggcct tcttagtgaa tgggccaatg attctagttt cagagtcttg gaaggatgaa 480

Aren0054.ST25.txt

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ggtagtgaat gtgaacctgg atttttttcg gaatggtaca tccttgccat cacatcattc 540
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ctgtggaagc gtgatcatct cagtaggtgc caaagccatc ctggactgac tgctgtctct 660
tccaacatct gtggacactc attcagaggt agactatctt caaggagatc tctttctgca 720
tcgacagaag ttcctgcata ctttcattca gagagacaga ggagaaagag tagtctcatg 780
ttttcctcaa gaaccaagat gaatagcaat acaattgctt ccaaaatggg ttccttctcc 840
caatcagatt ctgtagctct tcaccaaaagg gaacatggtg aactgcttag agccaggaga 900
ttagccaagt cactggccat tctcttaggg gtttttgctg ttgctgggc tccatattct 960
ctgttcacaa ttgtcctttc attttattcc tcagcaacag gtccctaaatc agtttggtat 1020
agaattgcat tttggcttca gtggttcaat tcctttgtca atcctctttt gtatccattg 1080
tgtcacaaagc gctttcaaaa ggctttcttg aaaatatattt gtataaaaaa gcaacctcta 1140
ccatcacaaac acagtcgggc agtatcttct taa 1173

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<210> 14  
 <211> 390  
 <212> PRT  
 <213> Homo sapiens

<400> 14

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Met Pro Asp Thr Asn Ser Thr Ile Asn Leu Ser Leu Ser Thr Arg Val
1          5          10          15
Thr Leu Ala Phe Phe Met Ser Leu Val Ala Phe Ala Ile Met Leu Gly
          20          25          30
Asn Ala Leu Val Ile Leu Ala Phe Val Val Asp Lys Asn Leu Arg His
          35          40          45
Arg Ser Ser Tyr Phe Phe Leu Asn Leu Ala Ile Ser Asp Phe Phe Val
          50          55          60
Gly Val Ile Ser Ile Pro Leu Tyr Ile Pro His Thr Leu Phe Glu Trp
65          70          75          80
Asp Phe Gly Lys Glu Ile Cys Val Phe Trp Leu Thr Thr Asp Tyr Leu
          85          90          95
Leu Cys Thr Ala Ser Val Tyr Asn Ile Val Leu Ile Ser Tyr Asp Arg
          100          105          110
Tyr Leu Ser Val Ser Asn Ala Val Ser Tyr Arg Thr Gln His Thr Gly
          115          120          125
Val Leu Lys Ile Val Thr Leu Met Val Ala Val Trp Val Leu Ala Phe
          130          135          140
Leu Val Asn Gly Pro Met Ile Leu Val Ser Glu Ser Trp Lys Asp Glu
          145          150          155          160
Gly Ser Glu Cys Glu Pro Gly Phe Phe Ser Glu Trp Tyr Ile Leu Ala
          165          170          175

```

Aren0054.ST25.txt

Ile Thr Ser Phe Leu Glu Phe Val Ile Pro Val Ile Leu Val Ala Tyr  
180 185 190

Phe Asn Met Asn Ile Tyr Trp Ser Leu Trp Lys Arg Asp His Leu Ser  
195 200 205

Arg Cys Gln Ser His Pro Gly Leu Thr Ala Val Ser Ser Asn Ile Cys  
210 215 220

Gly His Ser Phe Arg Gly Arg Leu Ser Ser Arg Arg Ser Leu Ser Ala  
225 230 235 240

Ser Thr Glu Val Pro Ala Ser Phe His Ser Glu Arg Gln Arg Arg Lys  
245 250 255

Ser Ser Leu Met Phe Ser Ser Arg Thr Lys Met Asn Ser Asn Thr Ile  
260 265 270

Ala Ser Lys Met Gly Ser Phe Ser Gln Ser Asp Ser Val Ala Leu His  
275 280 285

Gln Arg Glu His Val Glu Leu Leu Arg Ala Arg Arg Leu Ala Lys Ser  
290 295 300

Leu Ala Ile Leu Leu Gly Val Phe Ala Val Cys Trp Ala Pro Tyr Ser  
305 310 315 320

Leu Phe Thr Ile Val Leu Ser Phe Tyr Ser Ser Ala Thr Gly Pro Lys  
325 330 335

Ser Val Trp Tyr Arg Ile Ala Phe Trp Leu Gln Trp Phe Asn Ser Phe  
340 345 350

Val Asn Pro Leu Leu Tyr Pro Leu Cys His Lys Arg Phe Gln Lys Ala  
355 360 365

Phe Leu Lys Ile Phe Cys Ile Lys Lys Gln Pro Leu Pro Ser Gln His  
370 375 380

Ser Arg Ser Val Ser Ser  
385 390

<210> 15  
<211> 30  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 15  
ggaaagctta acgatcccca ggagcaacat

30

<210> 16  
<211> 31  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 16  
ctgggatcct acgagagcat ttttcacaca g

31



Aren0054.ST25.txt

<210> 17  
 <211> 1128  
 <212> DNA  
 <213> Homo sapiens

<400> 17  
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 aagctggcca cgctcagcct gctgctgtgc gtgagcctag cgggcaacgt gctgttcgcg 120  
 ctgctgatcg tgcgggagcg cagcctgcac cgcgcccggt actacctgct gctcgacctg 180  
 tgcctggccg acggggtcgc cgcgctcgcc tgcctcccg cgcctcatgct ggcggcgcg 240  
 cgtgcggcgg ccgcggcggg ggcgcgcgcg ggcgcgctgg gctgcaagct gctcgccctc 300  
 ctggcgcgcg tcttctgctt ccacgcgcgc ttcctgctgc tgggcgtggg cgtcaccgcg 360  
 tacctggcca tcgcgcacca ccgcttctat gcagagcgcc tggccggctg gccgtgcgc 420  
 gccatgctgg tgtgcgccgc ctgggcgctg gcgctggccg cggccttccc gccagtgtg 480  
 gacggcggtg gcgacgacga ggacgcgcgc tgcgccctgg agcagcggcc cgacggcgcc 540  
 cccggcgcg cgggcttctt gctgctgctg gccgtggtgg tgggcgccac gcacctcgtc 600  
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 cccgccgtca gccacgactg gaccttcac ggcccggcg ccaccggcca ggcggccgc 720  
 aactggacgg cgggcttcg ccgcgggccc acgccgccg cgcttggtgg catccggccc 780  
 gcagggcccg gccgcggcgc gcgcgcctc ctgctgctgg aagaattcaa gacggagaag 840  
 aggtgtgca agatgttcta cgcggtcac ctgctcttc tgcctctctg ggggccctac 900  
 gtcgtggcca gctacctgc ggtcctggtg cggcccgcg ccgtccccc ggcctacctg 960  
 acggcctccg tgtggctgac cttcgcgag gccggcatca acccgcgtgt gtgcttctc 1020  
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 accaccagg cgacccatcc ctgcgacctg aaaggcattg gtttatga 1128

<210> 18  
 <211> 375  
 <212> PRT  
 <213> Homo sapiens

<400> 18  
 Met Ala Asn Ala Ser Glu Pro Gly Gly Ser Gly Gly Gly Glu Ala Ala  
 1 5 10 15  
 Ala Leu Gly Leu Lys Leu Ala Thr Leu Ser Leu Leu Leu Cys Val Ser  
 20 25 30  
 Leu Ala Gly Asn Val Leu Phe Ala Leu Leu Ile Val Arg Glu Arg Ser  
 35 40 45  
 Leu His Arg Ala Pro Tyr Tyr Leu Leu Leu Asp Leu Cys Leu Ala Asp  
 50 55 60

## Aren0054.ST25.txt

Gly Leu Arg Ala Leu Ala Cys Leu Pro Ala Val Met Leu Ala Ala Arg  
 65 70 75 80  
 Arg Ala Ala Ala Ala Ala Gly Ala Pro Pro Gly Ala Leu Gly Cys Lys  
 85 90 95  
 Leu Leu Ala Phe Leu Ala Ala Leu Phe Cys Phe His Ala Ala Phe Leu  
 100 105 110  
 Leu Leu Gly Val Gly Val Thr Arg Tyr Leu Ala Ile Ala His His Arg  
 115 120 125  
 Phe Tyr Ala Glu Arg Leu Ala Gly Trp Pro Cys Ala Ala Met Leu Val  
 130 135 140  
 Cys Ala Ala Trp Ala Leu Ala Leu Ala Ala Ala Phe Pro Pro Val Leu  
 145 150 155 160  
 Asp Gly Gly Gly Asp Asp Glu Asp Ala Pro Cys Ala Leu Glu Gln Arg  
 165 170 175  
 Pro Asp Gly Ala Pro Gly Ala Leu Gly Phe Leu Leu Leu Leu Ala Val  
 180 185 190  
 Val Val Gly Ala Thr His Leu Val Tyr Leu Arg Leu Leu Phe Phe Ile  
 195 200 205  
 His Asp Arg Arg Lys Met Arg Pro Ala Arg Leu Val Pro Ala Val Ser  
 210 215 220  
 His Asp Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln Ala Ala Ala  
 225 230 235 240  
 Asn Trp Thr Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Ala Leu Val  
 245 250 255  
 Gly Ile Arg Pro Ala Gly Pro Gly Arg Gly Ala Arg Arg Leu Leu Val  
 260 265 270  
 Leu Glu Glu Phe Lys Thr Glu Lys Arg Leu Cys Lys Met Phe Tyr Ala  
 275 280 285  
 Val Thr Leu Leu Phe Leu Leu Leu Trp Gly Pro Tyr Val Val Ala Ser  
 290 295 300  
 Tyr Leu Arg Val Leu Val Arg Pro Gly Ala Val Pro Gln Ala Tyr Leu  
 305 310 315 320  
 Thr Ala Ser Val Trp Leu Thr Phe Ala Gln Ala Gly Ile Asn Pro Val  
 325 330 335  
 Val Cys Phe Leu Phe Asn Arg Glu Leu Arg Asp Cys Phe Arg Ala Gln  
 340 345 350  
 Phe Pro Cys Cys Gln Ser Pro Arg Thr Thr Gln Ala Thr His Pro Cys  
 355 360 365  
 Asp Leu Lys Gly Ile Gly Leu  
 370 375

<210> 19  
 <211> 1002  
 <212> DNA  
 <213> Homo sapiens

## Aren0054.ST25.txt

&lt;400&gt; 19

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aatacttttg ctctgtgggt gtttgttcac atccccagct cctccacctt catcatctac      180
ctcaaaaaca ctttggtggc cgacttgata atgacactca tgcttccttt caaaatcctc      240
tctgactcac acctggcacc ctggcagctc agagcttttg tgtgtcgttt ttcttcgggtg      300
atattttatg agaccatgta tgtgggcata gtgctgttag ggctcatagc ctttgacaga      360
ttcctcaaga tcatcagacc tttgagaaat atttttctaa aaaaacctgt ttttgcaaaa      420
acggtctcaa tcttcatctg gttctttttg ttcttcatct ccctgccaaa tacgatcttg      480
agcaacaagg aagcaacacc atcgtctgtg aaaaagtgtg cttccttaaa ggggcctctg      540
gggctgaaat ggcatacaat ggtaataaac atatgccagt ttattttctg gactgttttt      600
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tccaaaagta aggacagaaa aaacaacaaa aagctggaag gcaaagtatt tgtgtcgtg      720
gctgtcttct ttgtgtgttt tgctccattt ctttttgcca gagttccata tactcacagt      780
caaaccaaca ataagactga ctgtagactg caaaatcaac tgtttattgc taaagaaaca      840
actctctttt tggcagcaac taacatttgt atggatccct taatatacat attcttatgt      900
aaaaaattca cagaaaagct accatgtatg caagggagaa agaccacagc atcaagccaa      960
gaaaatcata gcagtcagac agacaacata accttaggct ga                          1002

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&lt;210&gt; 20

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 20

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Met Asn Thr Thr Val Met Gln Gly Phe Asn Arg Ser Glu Arg Cys Pro
1          5          10          15

Arg Asp Thr Arg Ile Val Gln Leu Val Phe Pro Ala Leu Tyr Thr Val
          20          25          30

Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu Ala Leu Trp Val Phe
          35          40          45

Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile Tyr Leu Lys Asn Thr
          50          55          60

Leu Val Ala Asp Leu Ile Met Thr Leu Met Leu Pro Phe Lys Ile Leu
          65          70          75          80

Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg Ala Phe Val Cys Arg
          85          90          95

Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr Val Gly Ile Val Leu
          100          105          110

Leu Gly Leu Ile Ala Phe Asp Arg Phe Leu Lys Ile Ile Arg Pro Leu

```

115

120

125

Arg Asn Ile Phe Leu Lys Lys Pro Val Phe Ala Lys Thr Val Ser Ile  
130 135 140

Phe Ile Trp Phe Phe Leu Phe Phe Ile Ser Leu Pro Asn Thr Ile Leu  
145 150 155 160

Ser Asn Lys Glu Ala Thr Pro Ser Ser Val Lys Lys Cys Ala Ser Leu  
165 170 175

Lys Gly Pro Leu Gly Leu Lys Trp His Gln Met Val Asn Asn Ile Cys  
180 185 190

Gln Phe Ile Phe Trp Thr Val Phe Ile Leu Met Leu Val Phe Tyr Val  
195 200 205

Val Ile Ala Lys Lys Val Tyr Asp Ser Tyr Arg Lys Ser Lys Ser Lys  
210 215 220

Asp Arg Lys Asn Asn Lys Lys Leu Glu Gly Lys Val Phe Val Val Val  
225 230 235 240

Ala Val Phe Phe Val Cys Phe Ala Pro Phe His Phe Ala Arg Val Pro  
245 250 255

Tyr Thr His Ser Gln Thr Asn Asn Lys Thr Asp Cys Arg Leu Gln Asn  
260 265 270

Gln Leu Phe Ile Ala Lys Glu Thr Thr Leu Phe Leu Ala Ala Thr Asn  
275 280 285

Ile Cys Met Asp Pro Leu Ile Tyr Ile Phe Leu Cys Lys Lys Phe Thr  
290 295 300

Glu Lys Leu Pro Cys Met Gln Gly Arg Lys Thr Thr Ala Ser Ser Gln  
305 310 315 320

Glu Asn His Ser Ser Gln Thr Asp Asn Ile Thr Leu Gly  
325 330

<210> 21  
<211> 1122  
<212> DNA  
<213> Homo sapiens

<400> 21  
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gccatcttgt ccctgctggt gctcaaggag cgtgccctgc acaaggctcc ttactacttc 180  
ctgctggacc tgtgcctggc cgatggcata cgctctgccg tctgctcccc ctttgtgctg 240  
gcttctgtgc gccacggctc ttcattggacc ttcagtgcac tcagctgcaa gattgtggcc 300  
tttatggccg tgctcttttg cttccatgcg gccttcattg tgttctgcat cagcgtcacc 360  
cgctacatgg ccacgcccc ccaccgcttc tacgccaagc gcatgacact ctggacatgc 420  
gcggctgtca tctgcatggc ctggaccctg tctgtggcca tggccttccc acctgtcttt 480  
gacgtgggca cctacaagtt tattcgggag gaggaccagt gcatctttga gcatcgctac 540

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ttcaaggcca atgacacgct gggcttcatg cttatgttgg ctgtgctcat ggcagctacc 600
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cagatggtgc cagccatcag ccagaactgg acattccatg gtcccggggc caccggccag 720
gctgctgcca actggatcgc cggctttggc cgtgggcccc tgccaccaac cctgctgggt 780
atccggcaga atgggcatgc agccagccgg cggctactgg gcatggacga ggtcaagggt 840
gaaaagcagc tgggcccgcg gttctacgcg atcacactgc tctttctgct cctctgggtca 900
ccctacatcg tggcctgcta ctggcgagtg tttgtgaaag cctgtgctgt gccccaccgc 960
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ggaggtgccc cggctcccag agaaccctac tgtgtcatgt ga 1122

```

```

<210> 22
<211> 373
<212> PRT
<213> Homo sapiens

```

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<400> 22

```

```

Met Ala Asn Thr Thr Gly Glu Pro Glu Glu Val Ser Gly Ala Leu Ser
1          5          10          15

```

```

Pro Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile
20          25          30

```

```

Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu
35          40          45

```

```

Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu
50          55          60

```

```

Cys Leu Ala Asp Gly Ile Arg Ser Ala Val Cys Phe Pro Phe Val Leu
65          70          75          80

```

```

Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys
85          90          95

```

```

Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe
100          105          110

```

```

Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His
115          120          125

```

```

Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Val Ile
130          135          140

```

```

Cys Met Ala Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Phe
145          150          155          160

```

```

Asp Val Gly Thr Tyr Lys Phe Ile Arg Glu Glu Asp Gln Cys Ile Phe
165          170          175

```

```

Glu His Arg Tyr Phe Lys Ala Asn Asp Thr Leu Gly Phe Met Leu Met
180          185          190

```

```

Leu Ala Val Leu Met Ala Ala Thr His Ala Val Tyr Gly Lys Leu Leu

```

195

200

Leu Phe Glu Tyr Arg His Arg Lys Met Lys Pro Val Gln Met Val Pro  
210 215 220

Ala Ile Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Thr Gly Gln  
225 230 235 240

Ala Ala Ala Asn Trp Ile Ala Gly Phe Gly Arg Gly Pro Met Pro Pro  
245 250 255

Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala Ala Ser Arg Arg Leu  
260 265 270

Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln Leu Gly Arg Met Phe  
275 280 285

Tyr Ala Ile Thr Leu Leu Phe Leu Leu Leu Trp Ser Pro Tyr Ile Val  
290 295 300

Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys Ala Val Pro His Arg  
305 310 315 320

Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala Gln Ala Ala Val Asn  
325 330 335

Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu Lys Lys Cys Leu Thr  
340 345 350

Thr His Ala Pro Cys Trp Gly Thr Gly Gly Ala Pro Ala Pro Arg Glu  
355 360 365

Pro Tyr Cys Val Met  
370

<210> 23  
<211> 1053  
<212> DNA  
<213> Homo sapiens

<400> 23  
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acttatgact acagtcaata tgaattgac tgtatcaaag aagatgtcag agaatttgca 120  
aaagttttcc tccctgtatt cctcacaata gctttcgtca ttggacttgc aggcaattcc 180  
atggtagtgg caatttatgc ctattacaag aaacagagaa caaaacaga tgtgtacatc 240  
ctgaatttgg ctgtagcaga ttactcctt ctattcactc tgcctttttg ggctgttaat 300  
gcagttcatg ggtgggtttt agggaaaata atgtgcaaaa taacttcagc cttgtacaca 360  
ctaaactttg tctctggaat gcagtttctg gcttgcatca gcatagacag atatgtggca 420  
gtaactaatg tccccagcca atcaggagtg ggaaaaccat gctggatcat ctgtttctgt 480  
gtctggatgg ctgccatctt gctgagcata cccagctgg ttttttatac agtaaagac 540  
aatgctaggt gcattcccat tttccccgc tacctaggaa catcaatgaa agcattgatt 600  
caaatgctag agatctgcat tggatttgta gtacccttct ttattatggg ggtgtgctac 660  
tttatcacgg caaggacact catgaagatg ccaaacatta aaatatctcg acccctaaaa 720

## Aren0054.ST25.txt

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gttctgctca cagtcgttat agttttcatt gtcactcaac tgccttataa cattgtcaag 780
ttctgccgag ccatagacat catctactcc ctgatcacca gctgcaacat gagcaaacgc 840
atggacatcg ccatccaagt cacagaaagc attgactctt ttcacagctg cctcaaccga 900
atccttttatg tttttatggg agcatctttc aaaaactacg ttatgaaagt ggccaagaaa 960
tatgggtcct ggagaagaca gagacaaagt gtggaggagt ttccttttga ttctgagggt 1020
cctacagagc caaccagtac ttttagcatt taa 1053

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<210> 24
<211> 350
<212> PRT
<213> Homo sapiens

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<400> 24

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Met Ala Leu Glu Gln Asn Gln Ser Thr Asp Tyr Tyr Tyr Glu Glu Asn
1          5          10          15

Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile
20          25          30

Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu
35          40          45

Thr Ile Ala Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala
50          55          60

Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile
65          70          75          80

Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Leu Phe Thr Leu Pro Phe
85          90          95

Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys
100         105         110

Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln
115         120         125

Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Asn Val
130         135         140

Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys
145         150         155         160

Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr
165         170         175

Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu
180         185         190

Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly
195         200         205

Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala
210         215         220

Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys
225         230         235         240

```

Aren0054.ST25.txt

Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr  
 245 250 255  
 Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile  
 260 265 270  
 Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr  
 275 280 285  
 Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val  
 290 295 300  
 Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys  
 305 310 315 320  
 Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe  
 325 330 335  
 Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile  
 340 345 350

<210> 25  
 <211> 1116  
 <212> DNA  
 <213> Homo sapiens

<400> 25  
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 gccaaagacct gcaacaacgt gtccttcgaa gagagcagga tagtcctggt cgtggtgtac 120  
 agcgcggtgt gcacgctggg ggtgccggcc aactgcctga ctgcgtggct ggcgctgctg 180  
 caggtactgc agggcaacgt gctggccgtc tacctgctct gcctggcact ctgcgaactg 240  
 ctgtacacag gcacgctgcc actctgggtc atctatatcc gcaaccagca ccgctggacc 300  
 ctaggcctgc tggcctcgaa ggtgaccgcc tacatcttct tctgcaacat ctacgtcagc 360  
 atcctcttcc tgtgctgcat ctctgctgac cgcttcgtgg ccgtggtgta cgcgctggag 420  
 agtcggggcc gccgccgccg gaggaccgcc atcctcatct ccgcctgcat cttcatcctc 480  
 gtcgggatcg ttcactaccc ggtgttccag acggaagaca aggagacctg ctttgacatg 540  
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 atgggcttaa gcgctgccca gaaggccaag gtgaagcact cggccatcgc ggtggtgtc 720  
 atcttcctag tctgcttcgc cccgtaccac ctggttctcc tcgtcaaagc cgctgccttt 780  
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 ctggccacgg accattcccg ccaagaagtg tccagaatcc ataaggggtg gaaagagtgg 960  
 tccatgaaga cagacgtcac caggtctacc cacagcaggg acaccgagga gctgcagtcg 1020  
 cccgtggccc ttgcagacca ctacaccttc tccaggcccg tgcacccacc agggtcacca 1080  
 tgccctgcaa agaggctgat tgaggagtcc tgctga 1116



<210> 26  
 <211> 371  
 <212> PRT  
 <213> Homo sapiens

<400> 26

Met Pro Gly Asn Ala Thr Pro Val Thr Thr Thr Ala Pro Trp Ala Ser  
 1 5 10 15

Leu Gly Leu Ser Ala Lys Thr Cys Asn Asn Val Ser Phe Glu Glu Ser  
 20 25 30

Arg Ile Val Leu Val Val Val Tyr Ser Ala Val Cys Thr Leu Gly Val  
 35 40 45

Pro Ala Asn Cys Leu Thr Ala Trp Leu Ala Leu Leu Gln Val Leu Gln  
 50 55 60

Gly Asn Val Leu Ala Val Tyr Leu Leu Cys Leu Ala Leu Cys Glu Leu  
 65 70 75 80

Leu Tyr Thr Gly Thr Leu Pro Leu Trp Val Ile Tyr Ile Arg Asn Gln  
 85 90 95

His Arg Trp Thr Leu Gly Leu Leu Ala Ser Lys Val Thr Ala Tyr Ile  
 100 105 110

Phe Phe Cys Asn Ile Tyr Val Ser Ile Leu Phe Leu Cys Cys Ile Ser  
 115 120 125

Cys Asp Arg Phe Val Ala Val Val Tyr Ala Leu Glu Ser Arg Gly Arg  
 130 135 140

Arg Arg Arg Arg Thr Ala Ile Leu Ile Ser Ala Cys Ile Phe Ile Leu  
 145 150 155 160

Val Gly Ile Val His Tyr Pro Val Phe Gln Thr Glu Asp Lys Glu Thr  
 165 170 175

Cys Phe Asp Met Leu Gln Met Asp Ser Arg Ile Ala Gly Tyr Tyr Tyr  
 180 185 190

Ala Arg Phe Thr Val Gly Phe Ala Ile Pro Leu Ser Ile Ile Ala Phe  
 195 200 205

Thr Asn His Arg Ile Phe Arg Ser Ile Lys Gln Ser Met Gly Leu Ser  
 210 215 220

Ala Ala Gln Lys Ala Lys Val Lys His Ser Ala Ile Ala Val Val Val  
 225 230 235 240

Ile Phe Leu Val Cys Phe Ala Pro Tyr His Leu Val Leu Leu Val Lys  
 245 250 255

Ala Ala Ala Phe Ser Tyr Tyr Arg Gly Asp Arg Asn Ala Met Cys Gly  
 260 265 270

Leu Glu Glu Arg Leu Tyr Thr Ala Ser Val Val Phe Leu Cys Leu Ser  
 275 280 285

Thr Val Asn Gly Val Ala Asp Pro Ile Ile Tyr Val Leu Ala Thr Asp  
 290 295 300

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His Ser Arg Gln Glu Val Ser Arg Ile His Lys Gly Trp Lys Glu Trp  
305 310 315 320

Ser Met Lys Thr Asp Val Thr Arg Leu Thr His Ser Arg Asp Thr Glu  
325 330 335

Glu Leu Gln Ser Pro Val Ala Leu Ala Asp His Tyr Thr Phe Ser Arg  
340 345 350

Pro Val His Pro Pro Gly Ser Pro Cys Pro Ala Lys Arg Leu Ile Glu  
355 360 365

Glu Ser Cys  
370

<210> 27  
<211> 1113  
<212> DNA  
<213> Homo sapiens

<400> 27  
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atctccattt tgctagtga agataagacc ttgcatagag caccttacta cttcctgttg 180  
gatctttgct gttcagatat cctcagatct gcaatttggt tcccatttgt gttcaactct 240  
gtcaaaaatg gctctacctg gacttatggg actctgactt gcaaagtgat tgcctttctg 300  
ggggttttgt cctgtttcca cactgctttc atgctcttct gcatcagtgt caccagatac 360  
ttagctatcg cccatcacccg cttctataca aagaggctga ccttttgac gtgtctggct 420  
gtgatctgta tgggtgtggac tctgtctgtg gccatggcat ttccccggg tttagacgtg 480  
ggcacttact cattcattag ggaggaagat caatgcacct tccaacaccg ctccttcagg 540  
gctaattgatt ccttaggatt tatgtctgctt cttgtctctca tctcctagc cacacagctt 600  
gtctacctca agctgatatt ttctgtccac gatcgaagaa aaatgaagcc agtccagttt 660  
gtagcagcag tcagccagaa ctggactttt catgggtcctg gagccagtgg ccaggcagct 720  
gccaattggc tagcaggatt tggaaggggt cccacaccac ccaccttgct gggcatcagg 780  
caaaatgcaa acaccacagg cagaagaagg ctattggtct tagacgagtt caaaatggag 840  
aaaagaatca gcagaatggt ctatataatg acttttctgt ttctaacctt gtggggcccc 900  
tacctgggtg cctgttattg gagagttttt gcaagagggc ctgtagtacc agggggattt 960  
ctaacagctg ctgtctggat gagttttgcc caagcaggaa tcaatccttt tgtctgcatt 1020  
ttctcaaaca gggagctgag gcgctgtttc agcacaacc ttctttactg cagaaaatcc 1080  
aggttaccaaa gggaacctta ctgtgttata tga 1113

<210> 28  
<211> 370  
<212> PRT  
<213> Homo sapiens

&lt;400&gt; 28

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Met Ala Asn Tyr Ser His Ala Ala Asp Asn Ile Leu Gln Asn Leu Ser
1      5      10      15
Pro Leu Thr Ala Phe Leu Lys Leu Thr Ser Leu Gly Phe Ile Ile Gly
20      25      30
Val Ser Val Val Gly Asn Leu Leu Ile Ser Ile Leu Leu Val Lys Asp
35      40      45
Lys Thr Leu His Arg Ala Pro Tyr Tyr Phe Leu Leu Asp Leu Cys Cys
50      55      60
Ser Asp Ile Leu Arg Ser Ala Ile Cys Phe Pro Phe Val Phe Asn Ser
65      70      75      80
Val Lys Asn Gly Ser Thr Trp Thr Tyr Gly Thr Leu Thr Cys Lys Val
85      90      95
Ile Ala Phe Leu Gly Val Leu Ser Cys Phe His Thr Ala Phe Met Leu
100     105     110
Phe Cys Ile Ser Val Thr Arg Tyr Leu Ala Ile Ala His His Arg Phe
115     120     125
Tyr Thr Lys Arg Leu Thr Phe Trp Thr Cys Leu Ala Val Ile Cys Met
130     135     140
Val Trp Thr Leu Ser Val Ala Met Ala Phe Pro Pro Val Leu Asp Val
145     150     155     160
Gly Thr Tyr Ser Phe Ile Arg Glu Glu Asp Gln Cys Thr Phe Gln His
165     170     175
Arg Ser Phe Arg Ala Asn Asp Ser Leu Gly Phe Met Leu Leu Leu Ala
180     185     190
Leu Ile Leu Leu Ala Thr Gln Leu Val Tyr Leu Lys Leu Ile Phe Phe
195     200     205
Val His Asp Arg Arg Lys Met Lys Pro Val Gln Phe Val Ala Ala Val
210     215     220
Ser Gln Asn Trp Thr Phe His Gly Pro Gly Ala Ser Gly Gln Ala Ala
225     230     235     240
Ala Asn Trp Leu Ala Gly Phe Gly Arg Gly Pro Thr Pro Pro Thr Leu
245     250     255
Leu Gly Ile Arg Gln Asn Ala Asn Thr Thr Gly Arg Arg Arg Leu Leu
260     265     270
Val Leu Asp Glu Phe Lys Met Glu Lys Arg Ile Ser Arg Met Phe Tyr
275     280     285
Ile Met Thr Phe Leu Phe Leu Thr Leu Trp Gly Pro Tyr Leu Val Ala
290     295     300
Cys Tyr Trp Arg Val Phe Ala Arg Gly Pro Val Val Pro Gly Gly Phe
305     310     315     320
Leu Thr Ala Ala Val Trp Met Ser Phe Ala Gln Ala Gly Ile Asn Pro
325     330     335

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Aren0054.ST25.txt

Phe Val Cys Ile Phe Ser Asn Arg Glu Leu Arg Arg Cys Phe Ser Thr  
340 345 350

Thr Leu Leu Tyr Cys Arg Lys Ser Arg Leu Pro Arg Glu Pro Tyr Cys  
355 360 365

Val Ile  
370

<210> 29  
<211> 1080  
<212> DNA  
<213> Homo sapiens

<400> 29  
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aacctcttct ctctgtgggt gctgtgccgg cgcattggggc ccagatcccc gtcggtcatc 180  
ttcatgatca acctgagcgt cacggacctg atgctggcca gcgtgttgcc tttccaaatc 240  
tactaccatt gcaaccgcca cactgggta ttcgggtgct tgccttgcaa cgtggtgacc 300  
gtggcctttt acgcaaactat gtattccagc atcctcacca tgacctgtat cagcgtggag 360  
cgcttcctgg gggctcctgta cccgctcagc tccaagcgtt ggcgcgcgcg tcgttacgcg 420  
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accgatctca cctaccgggt gcacgccctg ggcatcatca cctgcttcga cgtcctcaag 540  
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gtggtcttgc tggcctttgt cacctgcttc gcccccaaca acttcgtgct cctggcgcac 780  
atcgtgagcc gcctgttcta cggcaagagc tactaccagc tgtacaagct cacgctgtgt 840  
ctcagctgcc tcaacaactg tctggaccog tttgtttatt actttgcgtc ccggaattc 900  
cagctgcgcc tgcgggaata tttgggctgc cgccgggtgc ccagagacac cctggacacg 960  
cgccgcgaga gcctcttctc cgccaggacc acgtccgtgc gctccaggc cgggtgcgcac 1020  
cctgaaggga tggagggagc caccaggccc ggctccaga ggcaggagag tgtgttctga 1080

<210> 30  
<211> 359  
<212> PRT  
<213> Homo sapiens

<400> 30

Met Gln Val Pro Asn Ser Thr Gly Pro Asp Asn Ala Thr Leu Gln Met  
1 5 10 15

Leu Arg Asn Pro Ala Ile Ala Val Ala Leu Pro Val Val Tyr Ser Leu  
20 25 30

## Aren0054.ST25.txt

Val Ala Ala Val Ser Ile Pro Gly Asn Leu Phe Ser Leu Trp Val Leu  
 35 40 45  
 Cys Arg Arg Met Gly Pro Arg Ser Pro Ser Val Ile Phe Met Ile Asn  
 50 55 60  
 Leu Ser Val Thr Asp Leu Met Leu Ala Ser Val Leu Pro Phe Gln Ile  
 65 70 75 80  
 Tyr Tyr His Cys Asn Arg His His Trp Val Phe Gly Val Leu Leu Cys  
 85 90 95  
 Asn Val Val Thr Val Ala Phe Tyr Ala Asn Met Tyr Ser Ser Ile Leu  
 100 105 110  
 Thr Met Thr Cys Ile Ser Val Glu Arg Phe Leu Gly Val Leu Tyr Pro  
 115 120 125  
 Leu Ser Ser Lys Arg Trp Arg Arg Arg Tyr Ala Val Ala Ala Cys  
 130 135 140  
 Ala Gly Thr Trp Leu Leu Leu Leu Thr Ala Leu Cys Pro Leu Ala Arg  
 145 150 155 160  
 Thr Asp Leu Thr Tyr Pro Val His Ala Leu Gly Ile Ile Thr Cys Phe  
 165 170 175  
 Asp Val Leu Lys Trp Thr Met Leu Pro Ser Val Ala Met Trp Ala Val  
 180 185 190  
 Phe Leu Phe Thr Ile Phe Ile Leu Leu Phe Leu Ile Pro Phe Val Ile  
 195 200 205  
 Thr Val Ala Cys Tyr Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu  
 210 215 220  
 Glu Ala His Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala  
 225 230 235 240  
 Val Val Leu Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val  
 245 250 255  
 Leu Leu Ala His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr  
 260 265 270  
 His Val Tyr Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu  
 275 280 285  
 Asp Pro Phe Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu  
 290 295 300  
 Arg Glu Tyr Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr  
 305 310 315 320  
 Arg Arg Glu Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu  
 325 330 335  
 Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu  
 340 345 350  
 Gln Arg Gln Glu Ser Val Phe  
 355

&lt;210&gt; 31

&lt;211&gt; 1503

<212> DNA  
<213> Homo sapiens

<400> 31  
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ccagtcgccc cgggggcgcg ctccggtgcc gcggcgagtg gcacaggctg gcagccatgg 120  
gctgagtgcc cgggacccaa ggggaggggg caactgctgg cgaccgccgg ccttttgcgt 180  
cgctggcccc cccctcgcg tgcagctcc agccccgccc ccggagcggc gtccgctcac 240  
tcggttcaag gcagcgcgac tgcgggtggc gcacgaccag ggcgagacc ttggggcgcg 300  
cggcccatgg agtcggggct gctgcggccg gcgccggtga gcgaggtcat cgtcctgcat 360  
tacaactaca ccggcaagct ccgcggtgcg agctaccagc cgggtgccgg cctgcgcgcc 420  
gacgcgctgg tgtgcctggc ggtgtgcgcc ttcctcgtgc tagagaatct agccgtgttg 480  
ttggtgctcg gacgccaccc gcgcttccac gctcccatgt tcctgctcct gggcagcctc 540  
acgttgtcgg atctgctggc aggcgcgcgc tacgccgcca acatcctact gtcggggccg 600  
ctcacgctga aactgtcccc cgcgctctgg ttcgcacggg agggaggcgt cttcgtggca 660  
ctcactgcgt ccgtgctgag cctcctggcc atcgcgctgg agcgcagcct caccatggcg 720  
cgcagggggc ccgcgcccgt ctccagtcgg gggcgcacgc tggcgatggc agcccgggcc 780  
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ctcgccttcg tgggcatacct ggccgcgatc tgtgcaactc acgcgcgcat ctactgccag 960  
gtacgcgcca acgcgcggcg cctgccggca cggcccggga ctgcggggac cacctcgacc 1020  
cgggcgcgtc gcaagccgcg ctctctggcc ttgctgcgca cgctcagcgt ggtgctcctg 1080  
gcctttgtgg catgttgggg cccctcttc ctgctgctgt tgctcgacgt ggctgccccg 1140  
gcgcgcacct gtctgtact cctgcaggcc gatcccttc tgggactggc catggccaac 1200  
tcaattctga accccatcat ctacacgctc accaaccgcg acctgcgcca cgcgctcctg 1260  
cgctggtct gctgcggacg ccaactcctgc ggcagagacc cgagtggctc ccagcagtcg 1320  
gcgagcgcg ctagagcttc cgggggcctg cgccgctgcc tgccccggg ccttgatggg 1380  
agcttcagcg gctcggagcg ctcatcgccc cagcgcgacg ggctggacac cagcggctcc 1440  
acaggcagcc ccggtgcacc cacagccgcc cggactctgg tatcagaacc ggctgcagac 1500  
tga 1503

<210> 32  
<211> 500  
<212> PRT  
<213> Homo sapiens

<400> 32

Met Glu Arg Pro Trp Glu Asp Ser Pro Gly Pro Glu Gly Ala Ala Glu

1                    5                    10                    15  
 Gly Ser Pro Val Pro Val Ala Ala Gly Ala Arg Ser Gly Ala Ala Ala  
                   20                    25                    30  
 Ser Gly Thr Gly Trp Gln Pro Trp Ala Glu Cys Pro Gly Pro Lys Gly  
                   35                    40                    45  
 Arg Gly Gln Leu Leu Ala Thr Ala Gly Pro Leu Arg Arg Trp Pro Ala  
                   50                    55                    60  
 Pro Ser Pro Ala Ser Ser Ser Pro Ala Pro Gly Ala Ala Ser Ala His  
                   65                    70                    75                    80  
 Ser Val Gln Gly Ser Ala Thr Ala Gly Gly Ala Arg Pro Gly Arg Arg  
                   85                    90                    95  
 Pro Trp Gly Ala Arg Pro Met Glu Ser Gly Leu Leu Arg Pro Ala Pro  
                   100                    105                    110  
 Val Ser Glu Val Ile Val Leu His Tyr Asn Tyr Thr Gly Lys Leu Arg  
                   115                    120                    125  
 Gly Ala Ser Tyr Gln Pro Gly Ala Gly Leu Arg Ala Asp Ala Val Val  
                   130                    135                    140  
 Cys Leu Ala Val Cys Ala Phe Ile Val Leu Glu Asn Leu Ala Val Leu  
                   145                    150                    155                    160  
 Leu Val Leu Gly Arg His Pro Arg Phe His Ala Pro Met Phe Leu Leu  
                   165                    170                    175  
 Leu Gly Ser Leu Thr Leu Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala  
                   180                    185                    190  
 Ala Asn Ile Leu Leu Ser Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala  
                   195                    200                    205  
 Leu Trp Phe Ala Arg Glu Gly Gly Val Phe Val Ala Leu Thr Ala Ser  
                   210                    215                    220  
 Val Leu Ser Leu Leu Ala Ile Ala Leu Glu Arg Ser Leu Thr Met Ala  
                   225                    230                    235                    240  
 Arg Arg Gly Pro Ala Pro Val Ser Ser Arg Gly Arg Thr Leu Ala Met  
                   245                    250                    255  
 Ala Ala Ala Ala Trp Gly Val Ser Leu Leu Leu Gly Leu Leu Pro Ala  
                   260                    265                    270  
 Leu Gly Trp Asn Cys Leu Gly Arg Leu Asp Ala Cys Ser Thr Val Leu  
                   275                    280                    285  
 Pro Leu Tyr Ala Lys Ala Tyr Val Leu Phe Cys Val Leu Ala Phe Val  
                   290                    295                    300  
 Gly Ile Leu Ala Ala Ile Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln  
                   305                    310                    315                    320  
 Val Arg Ala Asn Ala Arg Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly  
                   325                    330                    335  
 Thr Thr Ser Thr Arg Ala Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu  
                   340                    345                    350

Aren0054.ST25.txt

Arg Thr Leu Ser Val Val Leu Leu Ala Phe Val Ala Cys Trp Gly Pro  
355 360 365

Leu Phe Leu Leu Leu Leu Leu Asp Val Ala Cys Pro Ala Arg Thr Cys  
370 375 380

Pro Val Leu Leu Gln Ala Asp Pro Phe Leu Gly Leu Ala Met Ala Asn  
385 390 395 400

Ser Leu Leu Asn Pro Ile Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg  
405 410 415

His Ala Leu Leu Arg Leu Val Cys Cys Gly Arg His Ser Cys Gly Arg  
420 425 430

Asp Pro Ser Gly Ser Gln Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly  
435 440 445

Gly Leu Arg Arg Cys Leu Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly  
450 455 460

Ser Glu Arg Ser Ser Pro Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser  
465 470 475 480

Thr Gly Ser Pro Gly Ala Pro Thr Ala Ala Arg Thr Leu Val Ser Glu  
485 490 495

Pro Ala Ala Asp  
500

<210> 33  
<211> 1029  
<212> DNA  
<213> Homo sapiens

<400> 33  
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tacaaaaatca cccaggtcct cttcccactg ctctacactg tcctgttttt tgttggaactt 120  
atcacaaatg gcctggcgat gaggattttc tttcaaattc ggagtaaadc aaactttatt 180  
atttttctta agaacacagt catttctgat cttctcatga ttctgacttt tccattcaaa 240  
attcttagtg atgccaaact gggaacagga ccaactgagaa cttttgtgtg tcaagttacc 300  
tccgtcatat tttatttcac aatgtatatc agtatttcat tcctgggact gataactatc 360  
gatcgctacc agaagaccac caggccattt aaaacatcca accccaaaaa tctcttgggg 420  
gctaagattc tctctgttgt catctgggca ttcattgttct tactctcttt gcctaactg 480  
attctgacca acaggcagcc gagagacaag aatgtgaaga aatgctcttt ccttaaatca 540  
gagttcggtc tagtctggca tgaaatagta aattacatct gtcaagtcatt tttctggatt 600  
aatttcttaa ttgttattgt atgttatata ctcattacaa aagaactgta ccggtcatac 660  
gtaagaacga ggggtgtagg taaagtcccc aggaaaaagg tgaacgtcaa agttttcatt 720  
atcattgctg tattctttat ttgttttggt cttttccatt ttgcccgaat tccttacacc 780  
ctgagccaaa cccgggatgt ctttgactgc actgctgaaa atactctgtt ctatgtgaaa 840  
gagagcactc tgtggttaac ttccttaaatt gcatgcctgg atccgttcat ctattttttc 900



```

ctttgcaagt ccttcagaaa ttccttgata agtatgctga agtgcccaaa ttctgcaaca    960
tctctgtccc aggacaatag gaaaaaagaa caggatgggtg gtgacccaaa tgaagagact    1020
ccaatgtaa                                1029

```

```

<210> 34
<211> 342
<212> PRT
<213> Homo sapiens

```

```

<400> 34

```

```

Met Gln Ala Val Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu
1          5          10          15

```

```

Cys Thr Arg Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr
          20          25          30

```

```

Thr Val Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg
          35          40          45

```

```

Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys
50          55          60

```

```

Asn Thr Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys
65          70          75          80

```

```

Ile Leu Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val
          85          90          95

```

```

Cys Gln Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile
          100          105          110

```

```

Ser Phe Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg
          115          120          125

```

```

Pro Phe Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu
          130          135          140

```

```

Ser Val Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met
145          150          155          160

```

```

Ile Leu Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser
          165          170          175

```

```

Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr
          180          185          190

```

```

Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys
          195          200          205

```

```

Tyr Thr Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg
          210          215          220

```

```

Gly Val Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile
225          230          235          240

```

```

Ile Ile Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg
          245          250          255

```

```

Ile Pro Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala
          260          265          270

```

Aren0054.ST25.txt

Glu Asn Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser  
 275 280 285  
 Leu Asn Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser  
 290 295 300  
 Phe Arg Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr  
 305 310 315 320  
 Ser Leu Ser Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro  
 325 330 335  
 Asn Glu Glu Thr Pro Met  
 340

<210> 35  
 <211> 1077  
 <212> DNA  
 <213> Homo sapiens

<400> 35  
 atgtcgggtct gctaccgtcc cccaggggaac gagacactgc tgagctggaa gacttcgcgg 60  
 gccacaggca cagccttcct gctgctggcg gcgctgctgg ggctgcctgg caacggcttc 120  
 gtggtgtgga gcttggcggg ctggcggcct gcacgggggc gaccgctggc ggccacgctt 180  
 gtgctgcacc tggcgctggc cgacggcgcg gtgctgctgc tcacgccgct ctttgtggcc 240  
 ttctgaccc ggtaggctg gccgctgggc caggcgggct gcaaggcgggt gtactacgtg 300  
 tgcgcgctca gcatgtacgc cagcgtgctg ctaccggcc tgctcagcct gcagcgctgc 360  
 ctgcagtc cccgcccctt cctggcgctt cggtgcgca gcccgccctt ggcccgcgc 420  
 ctgctgctgg cggctctggt ggccgcccctg ttgctcgccg tcccggccgc cgtctaccgc 480  
 cacctgtgga gggaccgct atgccagctg tgccaccgt cgccggtcca cgccgccgc 540  
 cacctgagcc tggagactct gaccgctttc gtgcttcctt tcgggctgat gctcggctgc 600  
 tacagcgtga cgctggcacg gctgcggggc gccgctggg gctccgggcg gcacggggcg 660  
 cgggtgggccc ggctggtgag cgccatcgtg cttgccttcg gcttgctctg ggccccctac 720  
 cacgcagtca accttctgca ggcggtcgca gcgctggctc caccggaagg ggccttggcg 780  
 aagctgggcg gagccggcca ggcggcgca gcgggaacta cggccttggc cttcttcagt 840  
 tctagcgtca accgggtgct ctacgtcttc accgctggag atctgctgcc ccgggcaggt 900  
 cccgctttcc tcacgcggt cttcgaaggc tctggggagg ccgaggggg cgccgctct 960  
 agggaaggga ccatggagct ccgaactacc cctcagctga aagtgggtgg gcagggccgc 1020  
 ggcaatggag acccgggggg tgggatggag aaggacggtc cggaatggga cctttga 1077

<210> 36  
 <211> 358  
 <212> PRT  
 <213> Homo sapiens

<400> 36

## Aren0054.ST25.txt

Met Ser Val Cys Tyr Arg Pro Pro Gly Asn Glu Thr Leu Leu Ser Trp  
 1 5 10 15  
 Lys Thr Ser Arg Ala Thr Gly Thr Ala Phe Leu Leu Leu Ala Ala Leu  
 20 25 30  
 Leu Gly Leu Pro Gly Asn Gly Phe Val Val Trp Ser Leu Ala Gly Trp  
 35 40 45  
 Arg Pro Ala Arg Gly Arg Pro Leu Ala Ala Thr Leu Val Leu His Leu  
 50 55 60  
 Ala Leu Ala Asp Gly Ala Val Leu Leu Leu Thr Pro Leu Phe Val Ala  
 65 70 75 80  
 Phe Leu Thr Arg Gln Ala Trp Pro Leu Gly Gln Ala Gly Cys Lys Ala  
 85 90 95  
 Val Tyr Tyr Val Cys Ala Leu Ser Met Tyr Ala Ser Val Leu Leu Thr  
 100 105 110  
 Gly Leu Leu Ser Leu Gln Arg Cys Leu Ala Val Thr Arg Pro Phe Leu  
 115 120 125  
 Ala Pro Arg Leu Arg Ser Pro Ala Leu Ala Arg Arg Leu Leu Leu Ala  
 130 135 140  
 Val Trp Leu Ala Ala Leu Leu Leu Ala Val Pro Ala Ala Val Tyr Arg  
 145 150 155 160  
 His Leu Trp Arg Asp Arg Val Cys Gln Leu Cys His Pro Ser Pro Val  
 165 170 175  
 His Ala Ala Ala His Leu Ser Leu Glu Thr Leu Thr Ala Phe Val Leu  
 180 185 190  
 Pro Phe Gly Leu Met Leu Gly Cys Tyr Ser Val Thr Leu Ala Arg Leu  
 195 200 205  
 Arg Gly Ala Arg Trp Gly Ser Gly Arg His Gly Ala Arg Val Gly Arg  
 210 215 220  
 Leu Val Ser Ala Ile Val Leu Ala Phe Gly Leu Leu Trp Ala Pro Tyr  
 225 230 235 240  
 His Ala Val Asn Leu Leu Gln Ala Val Ala Leu Ala Pro Pro Glu  
 245 250 255  
 Gly Ala Leu Ala Lys Leu Gly Gly Ala Gly Gln Ala Ala Arg Ala Gly  
 260 265 270  
 Thr Thr Ala Leu Ala Phe Phe Ser Ser Ser Val Asn Pro Val Leu Tyr  
 275 280 285  
 Val Phe Thr Ala Gly Asp Leu Leu Pro Arg Ala Gly Pro Arg Phe Leu  
 290 295 300  
 Thr Arg Leu Phe Glu Gly Ser Gly Glu Ala Arg Gly Gly Gly Arg Ser  
 305 310 315 320  
 Arg Glu Gly Thr Met Glu Leu Arg Thr Thr Pro Gln Leu Lys Val Val  
 325 330 335  
 Gly Gln Gly Arg Gly Asn Gly Asp Pro Gly Gly Gly Met Glu Lys Asp

340

345

350

Gly Pro Glu Trp Asp Leu  
355

<210> 37  
<211> 1005  
<212> DNA  
<213> Homo sapiens

<400> 37  
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ctggaaaagt actacctttc ctttttttat gggattgagt tcgttggtgg agtccttgga 120  
aataccattg ttgtttacgg ctacatcttc tctctgaaga actggaacag cagtaatatt 180  
tatctcttta acctctctgt ctctgactta gcttttctgt gcaccctccc catgctgata 240  
aggagttatg ccaatggaaa ctggatatat ggagacgtgc tctgcataag caaccgatat 300  
gtgcttcatg ccaacctcta taccagcatt ctctttctca cttttatcag catagatcga 360  
tacttgataa ttaagtatcc tttccgagaa caccttctgc aaaagaaaga gtttgctatt 420  
ttaatctcct tggccatttg ggttttagta accttagagt tactacccat acttcccctt 480  
ataaatcctg ttataactga caatggcacc acctgtaatg attttgcaag ttctggagac 540  
cccaactaca acctcattta cagcatgtgt ctaacactgt tggggttcct tattcctctt 600  
tttgatgtgt gtttctttta ttacaagatt gctctcttcc taaagcagag gaataggcag 660  
gttgctactg ctctgcccct tgaaaagcct ctcaacttgg tcatcatggc agtggtaatc 720  
ttctctgtgc tttttacacc ctatcacgtc atgcggaatg tgaggatcgc ttcacgcctg 780  
gggagtggga agcagtatca gtgcactcag gtcgtcatca actcctttta cattgtgaca 840  
cggccttttg cctttctgaa cagtgtcatc aacctgtct tctattttct tttgggagat 900  
cacttcaggg acatgctgat gaatcaactg agacacaact tcaaaccct tacatccttt 960  
agcagatggg ctcatgaact cctactttca ttcagagaaa agtga 1005

<210> 38  
<211> 334  
<212> PRT  
<213> Homo sapiens

<400> 38

Met Leu Gly Ile Met Ala Trp Asn Ala Thr Cys Lys Asn Trp Leu Ala  
1 5 10 15  
Ala Glu Ala Ala Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile  
20 25 30  
Glu Phe Val Val Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr  
35 40 45  
Ile Phe Ser Leu Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn  
50 55 60

## Aren0054.ST25.txt

Leu Ser Val Ser Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile  
65 70 75 80

Arg Ser Tyr Ala Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile  
85 90 95

Ser Asn Arg Tyr Val Leu His Ala Asn Leu Tyr Thr Ser Ile Leu Phe  
100 105 110

Leu Thr Phe Ile Ser Ile Asp Arg Tyr Leu Ile Ile Lys Tyr Pro Phe  
115 120 125

Arg Glu His Leu Leu Gln Lys Lys Glu Phe Ala Ile Leu Ile Ser Leu  
130 135 140

Ala Ile Trp Val Leu Val Thr Leu Glu Leu Leu Pro Ile Leu Pro Leu  
145 150 155 160

Ile Asn Pro Val Ile Thr Asp Asn Gly Thr Thr Cys Asn Asp Phe Ala  
165 170 175

Ser Ser Gly Asp Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr  
180 185 190

Leu Leu Gly Phe Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr  
195 200 205

Lys Ile Ala Leu Phe Leu Lys Gln Arg Asn Arg Gln Val Ala Thr Ala  
210 215 220

Leu Pro Leu Glu Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile  
225 230 235 240

Phe Ser Val Leu Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile  
245 250 255

Ala Ser Arg Leu Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val  
260 265 270

Ile Asn Ser Phe Tyr Ile Val Thr Arg Pro Leu Ala Phe Leu Asn Ser  
275 280 285

Val Ile Asn Pro Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp  
290 295 300

Met Leu Met Asn Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe  
305 310 315 320

Ser Arg Trp Ala His Glu Leu Leu Leu Ser Phe Arg Glu Lys  
325 330

<210> 39

<211> 1296

<212> DNA

<213> Homo sapiens

<400> 39

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acgcgggagc agttcatcgc tctgtaccgg ctgcgaccgc tcgtctacac ccagagctg 120

ccgggacgcg ccaagctggc cctcgtgctc accggcgtgc tcatcttcgc cctggcgctc 180

tttggaatg ctctggtgtt ctacgtggtg accgcagca aggccatgcg caccgtcacc 240

## Aren0054.ST25.txt

```

aacatcttta tctgctcctt ggcgctcagt gacctgctca tcaccttctt ctgcattccc 300
gtcaccatgc tccagaacat ttccgacaac tggctggggg gtgctttcat ttgcaagatg 360
gtgccatttg tccagtctac cgctgttggt acagaaatgc tcactatgac ctgcattgct 420
gtggaaaggc accagggact tgtgcatcct tttaaaatga agtggcaata caccaaccga 480
agggctttca caatgctagg tgtggtctgg ctggtggcag tcatcgtagg atcacccatg 540
tggcacgtgc aacaacttga gatcaaatat gacttcctat atgaaaagga acacatctgc 600
tgcttagaag agtggaccag ccctgtgcac cagaagatct acaccacctt catccttgtc 660
atcctcttcc tcctgcctct tatggtgatg cttattctgt acagtaaaat tggttatgaa 720
ctttggataa agaaaagagt tggggatggt tcagtgcctc gaactattca tggaaaagaa 780
atgtccaaaa tagccaggaa gaagaaacga gctgtcatta tgatggtgac agtgggtggct 840
ctctttgctg tgtgctgggc accattccat gttgtccata tgatgattga atacagtaat 900
tttggaaagg aatatgatga tgtcacaatc aagatgattt ttgctatcgt gcaaattatt 960
ggattttcca actccatctg taatcccatt gtctatgcat ttatgaatga aaacttcaaa 1020
aaaaatgttt tgtctgcagt ttgttattgc atagtaaata aaaccttctc tccagcacia 1080
aggcatggaa attcaggaat tacaatgatg cggaagaaag caaagtttct cctcagagag 1140
aatccagtgg aggaaaccaa aggagaagca ttcagtgatg gcaacattga agtcaaattg 1200
tgtgaacaga cagaggagaa gaaaaagctc aaacgacatc ttgctctctt taggtctgaa 1260
ctggctgaga attctccttt agacagtggg cattaa 1296

```

```

<210> 40
<211> 431
<212> PRT
<213> Homo sapiens
<400> 40

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```

Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg
1          5          10          15
Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg
20          25          30
Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu
35          40          45
Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala
50          55          60
Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr
65          70          75          80
Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe
85          90          95
Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu
100         105         110

```

## Aren0054.ST25.txt

Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala  
115 120 125

Val Val Thr Glu Met Leu Thr Met Thr Cys Ile Ala Val Glu Arg His  
130 135 140

Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg  
145 150 155 160

Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val  
165 170 175

Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe  
180 185 190

Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro  
195 200 205

Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu  
210 215 220

Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu  
225 230 235 240

Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile  
245 250 255

His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Lys Arg Ala Val  
260 265 270

Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro  
275 280 285

Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu  
290 295 300

Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile  
305 310 315 320

Gly Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn  
325 330 335

Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val  
340 345 350

Asn Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr  
355 360 365

Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu  
370 375 380

Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu  
385 390 395 400

Cys Glu Gln Thr Glu Glu Lys Lys Lys Leu Lys Arg His Leu Ala Leu  
405 410 415

Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His  
420 425 430

<210> 41

<211> 24

<212> DNA

<213> Artificial

&lt;220&gt;

&lt;223&gt; Novel Sequence

&lt;400&gt; 41

ctgtgtacag cagttcgag agtg

24

&lt;210&gt; 42

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Novel Sequence

&lt;400&gt; 42

gagtgccagg cagagcaggt agac

24

&lt;210&gt; 43

&lt;211&gt; 31

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Novel Sequence

&lt;400&gt; 43

cccgaattcc tgcttgctcc cagcttgcc c

31

&lt;210&gt; 44

&lt;211&gt; 32

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Novel Sequence

&lt;400&gt; 44

tgtggatcct gctgtcaaag gtccattcc gg

32

&lt;210&gt; 45

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Novel Sequence

&lt;400&gt; 45

tcacaatgct aggtgtggtc

20

&lt;210&gt; 46

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Novel Sequence

&lt;400&gt; 46

tgcatagaca atgggattac ag

22



<210> 47  
 <211> 511  
 <212> DNA  
 <213> Homo sapiens

<400> 47  
 tcacaatgct aggtgtggtc tggctggtgg cagtcacgt aggatcacc atgtggcacg 60  
 tgcaacaact tgagatcaaa tatgacttcc tatatgaaaa ggaacacatc tgctgcttag 120  
 aagagtggac cagccctgtg caccagaaga tctacaccac cttcatcctt gtcacacctt 180  
 tcctcctgcc tcttatggtg atgcttattc tgtacgtaaa attggttatg aactttggat 240  
 aaagaaaaga gttggggatg gttcagtgtc tcgaactatt catggaaaag aaatgtccaa 300  
 aatagccagg aagaagaaac gagctgtcat tatgatggtg acagtgggtg ctctctttgc 360  
 tgtgtgctgg gcaccattcc atgttgtcca tatgatgatt gaatacagta attttgaaaa 420  
 ggaatatgat gatgtcacia tcaagatgat ttttgctatc gtgcaaatta ttggattttc 480  
 caactccatc tgtaatccca ttgtctatgc a 511

<210> 48  
 <211> 21  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Novel Sequence

<400> 48  
 ctgcttagaa gagtggacca g 21

<210> 49  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Novel Sequence

<400> 49  
 ctgtgcacca gaagatctac ac 22

<210> 50  
 <211> 21  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Novel Sequence

<400> 50  
 caaggatgaa ggtggtgtag a 21

<210> 51  
 <211> 23

<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 51  
gtgtagatct tctggtgcac agg

23

<210> 52  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 52  
gcaatgcagg tcatagtgag c

21

<210> 53  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 53  
tggagcatgg tgacgggaat gcagaag

27

<210> 54  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 54  
gtgatgagca ggctactgag cgccaag

27

<210> 55  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 55  
gcaatgcagg cgcttaacat tac

23

<210> 56  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 56  
ttgggttaca atctgaaggg ca 22

<210> 57  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 57  
actccgtgtc cagcaggact ctg 23

<210> 58  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 58  
tgcgtgttcc tggaccctca cgtg 24

<210> 59  
<211> 29  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 59  
caggccttgg attttaatgt cagggatgg 29

<210> 60  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 60  
ggagagtcag ctctgaaaga attcagg 27

<210> 61  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 61  
tgatgtgatg ccagatacta atagcac 27

<210> 62  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Novel Sequence

<400> 62  
 cctgattcat ttaggtgaga ttgagac

27

<210> 63  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Novel Sequence

<400> 63  
 cccaagcttc cccaggtgta tttgat

26

<210> 64  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Novel Sequence

<400> 64  
 gttggatcca cataatgcat tttctc

26

<210> 65  
 <211> 1080  
 <212> DNA  
 <213> Homo sapiens

<400> 65  
 atgattctca actcttctac tgaagatggt attaaaagaa tccaagatga ttgtcccaaa 60  
 gctggaaggc ataattacat atttgtcatg attcctactt tatacagtat catctttgtg 120  
 gtgggaatat ttggaaacag cttggtggtg atagtcattt acttttatat gaagctgaag 180  
 actgtggcca gtgtttttct tttgaattta gcaactggctg acttatgctt tttactgact 240  
 ttgccactat gggctgtcta cacagctatg gaataccgct ggcccttttg caattaccta 300  
 tgtaagattg cttcagccag cgtcagtttc aacctgtacg ctagtgtgtt tctactcacg 360  
 tgtctcagca ttgatcgata cctggctatt gttcacccaa tgaagtccg ccttcgacgc 420  
 acaatgcttg tagccaaagt cacctgcata atcatttggc tgctggcagg cttggccagt 480  
 ttgccagcta taatccatcg aaatgtatth ttcattgaga acaccaatat tacagtttgt 540  
 gctttccatt atgagtccca aaattcaacc cttccgatag ggctgggcct gacaaaaaat 600  
 atactgggtt tcctgtttcc ttttctgata attcttaciaa gttatactct tatttggaag 660  
 gccctaaaga aggcttatga aattcagaag aacaaaccaa gaaatgatga tatttttaag 720

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ataattatgg caattgtgct tttctttttc ttttctgga ttccccacca aatattcact 780
tttctggatg tattgattca actaggcatc atacgtgact gtagaattgc agatattgtg 840
gacacggcca tgcctatcac catttgtata gcttatttta acaattgcct gaatcctctt 900
ttttatggct ttctggggaa aaaatttaaa agatattttc tccagcttct aaaatatatt 960
ccccaaaaag ccaaatccca ctcaaacctt tcaacaaaaa tgagcacgct ttcctaccgc 1020
ccctcagata atgtaagctc atccaccaag aagcctgcac catgttttga ggttgagtga 1080

```

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<210> 66
<211> 359
<212> PRT
<213> Homo sapiens

```

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<400> 66
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Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp
1 5 10 15

```

```

Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro
20 25 30

```

```

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu
35 40 45

```

```

Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser
50 55 60

```

```

Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr
65 70 75 80

```

```

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe
85 90 95

```

```

Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu
100 105 110

```

```

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu
115 120 125

```

```

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val
130 135 140

```

```

Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser
145 150 155 160

```

```

Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn
165 170 175

```

```

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro
180 185 190

```

```

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe
195 200 205

```

```

Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys
210 215 220

```

```

Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys
225 230 235 240

```

Aren0054.ST25.txt

Ile Ile Met Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Ile Pro His  
245 250 255

Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg  
260 265 270

Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile  
275 280 285

Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe  
290 295 300

Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile  
305 310 315 320

Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr  
325 330 335

Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro  
340 345 350

Ala Pro Cys Phe Glu Val Glu  
355

<210> 67  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 67  
accatgggca gccctggaa cggcagc

27

<210> 68  
<211> 39  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 68  
agaaccacca ccagcaggac gcggacggtc tgccggtg

39

<210> 69  
<211> 39  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 69  
gtccgcgtcc tgctggtggt ggttctggca ttataatt

39

<210> 70  
<211> 33  
<212> DNA  
<213> Artificial

&lt;220&gt;

&lt;223&gt; Novel Sequence

&lt;400&gt; 70

cctggatcct tatcccatcg tcttcacgtt agc

33

&lt;210&gt; 71

&lt;211&gt; 26

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Novel Sequence

&lt;400&gt; 71

ctggaattct cctgccagca tgggtga

26

&lt;210&gt; 72

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Novel Sequence

&lt;400&gt; 72

gcaggatcct atattgcgtg ctctgtcccc

30

&lt;210&gt; 73

&lt;211&gt; 999

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

atggtgaact ccaccaccg tgggatgcac acttctctgc acctctggaa ccgcagcagt 60

tacagactgc acagcaatgc cagtgaagtc cttggaaaag gctactctga tggaggggtgc 120

tacgagcaac tttttgtctc tctgaggtg tttgtgactc tgggtgtcat cagcttgttg 180

gagaatatct tagtgattgt ggcaatagcc aagaacaaga atctgcattc acccatgtac 240

tttttcatct gcagcttggc tgtggctgat atgctggtga gcgtttcaaa tggatcagaa 300

accattatca tcaccctatt aaacagtaca gatacggatg cacagagttt cacagtgaat 360

attgataatg tcattgactc ggtgatctgt agtccttgc ttgcatccat ttgcagcctg 420

ctttcaattg cagtggacag gtactttact atcttctatg ctctccagta ccataacatt 480

atgacagtta agcgggttg gatcagcata agttgtatct gggcagcttg cacggtttca 540

ggcattttgt tcatcattta ctcatagat agtgctgtca tcatctgcct catcaccatg 600

ttcttcacca tgctggctct catggcttct ctctatgtcc acatgttctt gatggccagg 660

cttcacatta agaggattgc tgtcctcccc ggcactggtg ccatccgcca aggtgccaat 720

atgaaggag cgattacctt gaccatcctg attggcgtct ttgtgtctg ctgggcccc 780

ttcttctctc acttaatat ctacatctct tgtcctcaga atccatattg tgtgtgcttc 840

## Aren0054.ST25.txt

```

atgtctcact ttaacttgta tctcactctg atcatgtgta attcaatcat cgatcctctg 900
atztatgcac tccggagtca agaactgagg aaaaccttca aagagatcat ctgttgctat 960
cccctgggag gcctttgtga cttgtctagc agatattaa 999

```

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<210> 74
<211> 332
<212> PRT
<213> Homo sapiens

```

```

<400> 74

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Met Val Asn Ser Thr His Arg Gly Met His Thr Ser Leu His Leu Trp
1 5 10 15

```

```

Asn Arg Ser Ser Tyr Arg Leu His Ser Asn Ala Ser Glu Ser Leu Gly
20 25 30

```

```

Lys Gly Tyr Ser Asp Gly Gly Cys Tyr Glu Gln Leu Phe Val Ser Pro
35 40 45

```

```

Glu Val Phe Val Thr Leu Gly Val Ile Ser Leu Leu Glu Asn Ile Leu
50 55 60

```

```

Val Ile Val Ala Ile Ala Lys Asn Lys Asn Leu His Ser Pro Met Tyr
65 70 75 80

```

```

Phe Phe Ile Cys Ser Leu Ala Val Ala Asp Met Leu Val Ser Val Ser
85 90 95

```

```

Asn Gly Ser Glu Thr Ile Ile Ile Thr Leu Leu Asn Ser Thr Asp Thr
100 105 110

```

```

Asp Ala Gln Ser Phe Thr Val Asn Ile Asp Asn Val Ile Asp Ser Val
115 120 125

```

```

Ile Cys Ser Ser Leu Leu Ala Ser Ile Cys Ser Leu Leu Ser Ile Ala
130 135 140

```

```

Val Asp Arg Tyr Phe Thr Ile Phe Tyr Ala Leu Gln Tyr His Asn Ile
145 150 155 160

```

```

Met Thr Val Lys Arg Val Gly Ile Ser Ile Ser Cys Ile Trp Ala Ala
165 170 175

```

```

Cys Thr Val Ser Gly Ile Leu Phe Ile Ile Tyr Ser Asp Ser Ser Ala
180 185 190

```

```

Val Ile Ile Cys Leu Ile Thr Met Phe Phe Thr Met Leu Ala Leu Met
195 200 205

```

```

Ala Ser Leu Tyr Val His Met Phe Leu Met Ala Arg Leu His Ile Lys
210 215 220

```

```

Arg Ile Ala Val Leu Pro Gly Thr Gly Ala Ile Arg Gln Gly Ala Asn
225 230 235 240

```

```

Met Lys Gly Ala Ile Thr Leu Thr Ile Leu Ile Gly Val Phe Val Val
245 250 255

```

```

Cys Trp Ala Pro Phe Phe Leu His Leu Ile Phe Tyr Ile Ser Cys Pro
260 265 270

```



Aren0054.ST25.txt

Gln Asn Pro Tyr Cys Val Cys Phe Met Ser His Phe Asn Leu Tyr Leu  
275 280 285

Ile Leu Ile Met Cys Asn Ser Ile Ile Asp Pro Leu Ile Tyr Ala Leu  
290 295 300

Arg Ser Gln Glu Leu Arg Lys Thr Phe Lys Glu Ile Ile Cys Cys Tyr  
305 310 315 320

Pro Leu Gly Gly Leu Cys Asp Leu Ser Ser Arg Tyr  
325 330

<210> 75  
<211> 32  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 75  
ccgaagcttc gagctgagta aggcggcggg ct 32

<210> 76  
<211> 31  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 76  
gtggaattca tttgccctgc ctcaaccccc a 31

<210> 77  
<211> 1344  
<212> DNA  
<213> Homo sapiens

<400> 77  
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ctgtgccgcc cgggggcgcc tctcctcaac agcagcagtg tgggcaacct cagctgcgag 120  
ccccctcgca ttcgcggagc cgggacacga gaattggagc tggccattag aatcactctt 180  
tacgcagtga tcttctgat gagcgttgga ggaaatatgc tcatcatcgt ggtcctggga 240  
ctgagccgcc gcctgaggac tgtcaccaat gccttcctcc tctcactggc agtcagcgac 300  
ctcctgctgg ctgtggcttg catgcccttc accctcctgc ccaatctcat gggcacattc 360  
atctttggca ccgtcatctg caaggcgggt tcctacctca tgggggtgtc tgtgagtgtg 420  
tccacgctaa gcctcgtggc catcgcactg gagcgatata gcgccatctg ccgaccactg 480  
caggcacgag tgtggcagac gcgctccac gcggctcgcg tgattgtagc cacgtggctg 540  
ctgtccggac tactcatggt gccctacccc gtgtacactg tcgtgcaacc agtggggcct 600  
cgtgtgctgc agtgctgca tcgctggccc agtgcgcggg tccgccagac ctgggtccgta 660

## Aren0054.ST25.txt

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ctgctgcttc tgctcttggt cttcatccca ggtgtggtta tggccgtggc ctacgggctt 720
atctctcgcg agctctactt agggcttcgc tttgacggcg acagtgcag cgacagccaa 780
agcaggggcc gaaaccaagg cgggctgcca ggggctgttc accagaacgg gcgttgccgg 840
cctgagactg ggcggttg gcaagacagc gatggctgct acgtgcaact tccacgttcc 900
cggcctgccc tggagctgac ggcgctgacg gctcctgggc cgggatccgg ctcccggccc 960
accaggcca agctgctggc taagaagcgc gtggtgcgaa tgttgctggt gatcgttgtg 1020
cttttttttc tgtgttggtt gccagtttat agtgccaaca cgtggcgcgc ctttgatggc 1080
ccgggtgcac accgagcact ctcggtgct cctatctcct tcattcactt gctgagctac 1140
gcctcggcct gtgtcaaccc cctggtctac tgcttcatgc accgtcgctt tcgccaggcc 1200
tgcttgaaa cttgcgctcg ctgctgcccc cggcctccac gagctcgccc cagggtcttt 1260
cccgatgagg acctccac tccctccatt gcttcgctgt ccaggcttag ctacaccacc 1320
atcagcacac tgggccctgg ctga 1344

```

```

<210> 78
<211> 447
<212> PRT
<213> Homo sapiens

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<400> 78

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Met Glu Leu Leu Lys Leu Asn Arg Ser Val Gln Gly Thr Gly Pro Gly
1          5          10          15
Pro Gly Ala Ser Leu Cys Arg Pro Gly Ala Pro Leu Leu Asn Ser Ser
          20          25          30
Ser Val Gly Asn Leu Ser Cys Glu Pro Pro Arg Ile Arg Gly Ala Gly
          35          40          45
Thr Arg Glu Leu Glu Leu Ala Ile Arg Ile Thr Leu Tyr Ala Val Ile
          50          55          60
Phe Leu Met Ser Val Gly Gly Asn Met Leu Ile Ile Val Val Leu Gly
65          70          75          80
Leu Ser Arg Arg Leu Arg Thr Val Thr Asn Ala Phe Leu Leu Ser Leu
          85          90          95
Ala Val Ser Asp Leu Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu
          100          105          110
Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys
          115          120          125
Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Ser Thr Leu Ser
          130          135          140
Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu
145          150          155          160
Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val
          165          170          175

```

Aren0054.ST25.txt

Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr  
180 185 190

Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg  
195 200 205

Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu  
210 215 220

Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu  
225 230 235 240

Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp  
245 250 255

Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala  
260 265 270

Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Lys  
275 280 285

Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu  
290 295 300

Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro  
305 310 315 320

Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Val Arg Met Leu Leu  
325 330 335

Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala  
340 345 350

Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser  
355 360 365

Val Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys  
370 375 380

Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala  
385 390 395 400

Cys Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg  
405 410 415

Pro Arg Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Ser Ile Ala Ser  
420 425 430

Leu Ser Arg Leu Ser Tyr Thr Thr Ile Ser Thr Leu Gly Pro Gly  
435 440 445

<210> 79  
<211> 30  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 79  
tgcaagctta aaaaggaaaa aatgaacagc

30

<210> 80  
<211> 30

<212> DNA  
 <213> Artificial

<220>  
 <223> Novel Sequence

<400> 80  
 taaggatccc ttcccttcaa aacatccttg 30

<210> 81  
 <211> 1014  
 <212> DNA  
 <213> Homo sapiens

<400> 81  
 atgaacagca catgtattga agaacagcat gacctggatc actatttggt tcccattggt 60  
 tacatctttg tgattatagt cagcattcca gccaatattg gatctctgtg tgtgtctttc 120  
 ctgcaaccca agaaggaaag tgaactagga atttacctct tcagtttggtc actatcagat 180  
 ttactctatg cattaactct ccctttatgg attgattata cttggaataa agacaactgg 240  
 actttctctc ctgccttggt caaagggagt gcttttctca tgtacatgaa gttttacagc 300  
 agcacagcat tcctcacctg cattgccgtt gatcgggtatt tggctgttgt ctaccctttg 360  
 aagttttttt tcctaaggac aagaagaatt gcactcatgg tcagcctgtc catctggata 420  
 ttggaaacca tcttcaatgc tgtcatgttg tgggaagatg aaacagttgt tgaatattgc 480  
 gatgccgaaa agtctaattt tactttatgc tatgacaaat accctttaga gaaatggcaa 540  
 atcaacctca acttggtcag gacgtgtaca ggctatgcaa tacctttggt caccatcctg 600  
 atctgtaacc ggaaagtcta ccaagctgtg cggcacaata aagccacgga aaacaaggaa 660  
 aagaagagaa tcataaaact acttgtcagc atcacagtta cttttgtctt atgctttact 720  
 ccctttcatg tgatgttgct gattcgtgc attttagagc atgctgtgaa cttcgaagac 780  
 cacagcaatt ctgggaagcg aacttacaca atgtatagaa tcacggttgc attaacaagt 840  
 ttaaattgtg ttgctgatcc aattctgtac tgttttgta ccgaaacag aagatatgat 900  
 atgtggaata tattaaaatt ctgcactggg aggtgtaata catcaciaag acaaagaaaa 960  
 cgcatacttt ctgtgtctac aaaagatact atggaattag aggtccttga gtag 1014

<210> 82  
 <211> 337  
 <212> PRT  
 <213> Homo sapiens

<400> 82

Met Asn Ser Thr Cys Ile Glu Glu Gln His Asp Leu Asp His Tyr Leu  
 1 5 10 15

Phe Pro Ile Val Tyr Ile Phe Val Ile Ile Val Ser Ile Pro Ala Asn  
 20 25 30

Ile Gly Ser Leu Cys Val Ser Phe Leu Gln Pro Lys Lys Glu Ser Glu

35

40

Leu Gly Ile Tyr Leu Phe Ser Leu Ser Leu Ser Asp Leu Leu Tyr Ala  
50 55 60

Leu Thr Leu Pro Leu Trp Ile Asp Tyr Thr Trp Asn Lys Asp Asn Trp  
65 70 75 80

Thr Phe Ser Pro Ala Leu Cys Lys Gly Ser Ala Phe Leu Met Tyr Met  
85 90 95

Lys Phe Tyr Ser Ser Thr Ala Phe Leu Thr Cys Ile Ala Val Asp Arg  
100 105 110

Tyr Leu Ala Val Val Tyr Pro Leu Lys Phe Phe Phe Leu Arg Thr Arg  
115 120 125

Arg Ile Ala Leu Met Val Ser Leu Ser Ile Trp Ile Leu Glu Thr Ile  
130 135 140

Phe Asn Ala Val Met Leu Trp Glu Asp Glu Thr Val Val Glu Tyr Cys  
145 150 155 160

Asp Ala Glu Lys Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr Pro Leu  
165 170 175

Glu Lys Trp Gln Ile Asn Leu Asn Leu Phe Arg Thr Cys Thr Gly Tyr  
180 185 190

Ala Ile Pro Leu Val Thr Ile Leu Ile Cys Asn Arg Lys Val Tyr Gln  
195 200 205

Ala Val Arg His Asn Lys Ala Thr Glu Asn Lys Glu Lys Lys Arg Ile  
210 215 220

Ile Lys Leu Leu Val Ser Ile Thr Val Thr Phe Val Leu Cys Phe Thr  
225 230 235 240

Pro Phe His Val Met Leu Leu Ile Arg Cys Ile Leu Glu His Ala Val  
245 250 255

Asn Phe Glu Asp His Ser Asn Ser Gly Lys Arg Thr Tyr Thr Met Tyr  
260 265 270

Arg Ile Thr Val Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile  
275 280 285

Leu Tyr Cys Phe Val Thr Glu Thr Gly Arg Tyr Asp Met Trp Asn Ile  
290 295 300

Leu Lys Phe Cys Thr Gly Arg Cys Asn Thr Ser Gln Arg Gln Arg Lys  
305 310 315 320

Arg Ile Leu Ser Val Ser Thr Lys Asp Thr Met Glu Leu Glu Val Leu  
325 330 335

Glu

<210> 83

<211> 40

<212> DNA

<213> Artificial

<220>

<223> Novel Sequence

<400> 83  
caggaagaag aaacgagctg tcattatgat ggtgacagtg 40

<210> 84  
<211> 40  
<212> DNA  
<213> Artificial

<220>

<223> Novel Sequence

<400> 84  
cactgtcacc atcataatga cagctcgttt cttcttcctg 40

<210> 85  
<211> 30  
<212> DNA  
<213> Artificial

<220>

<223> Novel Sequence

<400> 85  
ggccaccggc agaccaaacg cgtcctgctg 30

<210> 86  
<211> 31  
<212> DNA  
<213> Artificial

<220>

<223> Novel Sequence

<400> 86  
ctccttcggt cctcctatcg ttgtcagaag t 31

<210> 87  
<211> 37  
<212> DNA  
<213> Artificial

<220>

<223> Novel Sequence

<400> 87  
ggaaaagaag agaataaaaa aactacttgt cagcatc 37

<210> 88  
<211> 31  
<212> DNA  
<213> Artificial

<220>

<223> Novel Sequence

<400> 88  
ctccttcggt cctcctatcg ttgtcagaag t 31

<210> 89  
 <211> 1080  
 <212> DNA  
 <213> Homo sapiens

<400> 89  
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 gtgggaatat ttggaaacag cttggtggtg atagtcattt acttttatat gaagctgaag 180  
 actgtggcca gtgtttttct tttgaattta gcactggctg acttatgctt tttactgact 240  
 ttgccactat gggctgtcta cacagctatg gaataccgct ggcccttttg caattaccta 300  
 tgtaagattg cttcagccag cgtcagtttc aacctgtacg ctagtgtgtt tctactcacg 360  
 tgtctcagca ttgatcgata cctggctatt gttcacccaa tgaagtcccg ccttcgacgc 420  
 acaatgcttg tagccaaagt cacctgcac atcatttggc tgctggcagg cttggccagt 480  
 ttgccagcta taatccatcg aaatgtattt ttcattgaga acaccaatat tacagtttgt 540  
 gctttccatt atgagtccca aaattcaacc cttccgatag ggctgggcct gaccaaaaat 600  
 atactgggtt tcctgtttcc tttctgatc attcttacia gttatactct tatttgaag 660  
 gccctaaaga aggcttatga aattcagaag aacaaaccaa gaaatgatga tattaanaag 720  
 ataattatgg caattgtgct tttctttttc ttttctgga tttccaccca aatattcact 780  
 tttctggatg tattgattca actaggcatc atacgtgact gtagaattgc agatattgtg 840  
 gacacggcca tgcctatcac catttgtata gcttatttta acaattgcct gaatcctctt 900  
 ttttatggct ttctggggaa aaaatttaaa agatattttc tccagcttct aaaatatatt 960  
 cccccaaaag ccaaatccca ctcaaacctt tcaacaaaaa tgagcacgct ttctaccgc 1020  
 ccctcagata atgtaagctc atccaccaag aagcctgcac catgttttga gggtgagtga 1080

<210> 90  
 <211> 359  
 <212> PRT  
 <213> Homo sapiens

<400> 90  
 Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp  
 1 5 10 15  
 Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro  
 20 25 30  
 Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu  
 35 40 45  
 Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser  
 50 55 60  
 Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr  
 65 70 75 80

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Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe  
85 90 95

Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu  
100 105 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu  
115 120 125

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val  
130 135 140

Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser  
145 150 155 160

Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn  
165 170 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro  
180 185 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe  
195 200 205

Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys  
210 215 220

Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Lys Lys  
225 230 235 240

Ile Ile Met Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Ile Pro His  
245 250 255

Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg  
260 265 270

Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile  
275 280 285

Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe  
290 295 300

Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile  
305 310 315 320

Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr  
325 330 335

Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro  
340 345 350

Ala Pro Cys Phe Glu Val Glu  
355

<210> 91  
<211> 35  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 91  
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<210> 92  
 <211> 31  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Novel Sequence

<400> 92  
 ctccttcggt cctcctatcg ttgtcagaag t 31

<210> 93  
 <211> 1080  
 <212> DNA  
 <213> Homo sapiens

<400> 93  
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 gctggaaggc ataattacat atttgtcatg attcctactt tatacagtat catctttgtg 120  
 gtgggaatat ttggaaacag cttgggtggtg atagtcattt acttttatat gaagctgaag 180  
 actgtggcca gtgtttttct tttgaattta gcactggctg acttatgctt tttactgact 240  
 ttgccactat gggctgtcta cacagctatg gaataccgct ggcccttttg caattaccta 300  
 tgtaagattg cttcagccag cgtcagtttc gccctgtacg ctagtgtgtt tctactcag 360  
 tgtctcagca ttgatcgata cctggctatt gttcacccaa tgaagtcccg ccttcgacgc 420  
 acaatgcttg tagccaaagt cacctgcac atcatttggc tgctggcagg cttggccagt 480  
 ttgccagcta taatccatcg aaatgtattt ttcattgaga acaccaatat tacagtttgt 540  
 gctttccatt atgagtccca aaattcaacc cttccgatag ggctgggcct gacaaaaaat 600  
 atactgggtt tctgtttcc ttttctgac atctttacaa gttatactct tatttggaag 660  
 gccctaaaga aggcttatga aattcagaag aacaaaccaa gaaatgatga tatttttaag 720  
 ataattatgg caattgtgct tttctttttc ttttctgga ttccccacca aatattcact 780  
 tttctggatg tattgattca actaggcatc atacgtgact gtagaattgc agatattgtg 840  
 gacacggcca tgcctatcac catttgtata gcttatttta acaattgcct gaatcctctt 900  
 ttttatggct ttctggggaa aaaatttaaa agatattttc tccagcttct aaaatatatt 960  
 ccccaaaaag ccaaattcca ctcaaacctt tcaacaaaaa tgagcacgct ttcctaccgc 1020  
 ccctcagata atgtaagctc atccaccaag aagcctgcac catgttttga ggttgagtga 1080

<210> 94  
 <211> 359  
 <212> PRT  
 <213> Homo sapiens

<400> 94

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp

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1           5           10           15
Asp Cys Pro  Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro
      20           25           30
Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu
      35           40           45
Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser
      50           55           60
Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr
      65           70           75           80
Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe
      85           90           95
Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Ala Leu
      100          105          110
Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu
      115          120          125
Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val
      130          135          140
Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser
      145          150          155          160
Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn
      165          170          175
Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro
      180          185          190
Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe
      195          200          205
Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys
      210          215          220
Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys
      225          230          235          240
Ile Ile Met Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Ile Pro His
      245          250          255
Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg
      260          265          270
Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile
      275          280          285
Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe
      290          295          300
Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile
      305          310          315          320
Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr
      325          330          335
Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro
      340          345          350

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Ala Pro Cys Phe Glu Val Glu  
355

<210> 95  
<211> 26  
<212> DNA  
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<223> Novel Sequence

<400> 95  
cccaagcttc cccaggtgta ttgat

26

<210> 96  
<211> 29  
<212> DNA  
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<220>  
<223> Novel Sequence

<400> 96  
cctgcaggcg aaactgactc tggctgaag

29

<210> 97  
<211> 42  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 97  
ctgtacgcta gtgtgtttct actcacgtgt ctcagcattg at

42

<210> 98  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 98  
gttgatcca cataatgcat tttctc

26

<210> 99  
<211> 1080  
<212> DNA  
<213> Homo sapiens

<400> 99  
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gctggaaggc ataattacat atttgcacg attcctactt tatacagtat catctttgtg 120  
gtgggaatat ttggaaacag cttgggtggtg atagtcattt acttttatat gaagctgaag 180  
actgtggcca gtgtttttct tttgaattta gcactggctg acttatgctt tttactgact 240

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ttgccactat gggctgtcta cacagctatg gaataccgct ggccttttg caattaccta 300
tgtaagattg cttcagccag cgtcagtttc aacctgtacg ctagtgtgtt tctactcacg 360
tgtctcagca ttgatcgata cctggctatt gttcacccaa tgaagtcccg ccttcgacgc 420
acaatgcttg tagccaaagt cacctgcata atcatttggc tgctggcagg cttggccagt 480
ttgccagcta taatccatcg aaatgtattt ttcattgaga acaccaatat tacagtttgt 540
gttttccatt atgagtccca aaattcaacc cttccgatag ggctgggcct gaccaaaaat 600
atactgggtt tcctgtttcc tttctgatac attcttaciaa gttatttttg aattcgaaaa 660
cacttactga agacgaatag ctatgggaag aacaggataa cccgtgacca agttaagaag 720
ataattatgg caattgtgct tttctttttc ttttctgga ttccccacca aatattcact 780
tttctggatg tattgattca actaggcatc atacgtgact gtagaattgc agatattgtg 840
gacacggcca tgcctatcac catttgtata gcttatttta acaattgcct gaatcctctt 900
ttttatggct ttctggggaa aaaatttaaa agatattttc tccagcttct aaaatatatt 960
cccccaaaag ccaaatccca ctcaaacctt tcaacaaaaa tgagcacgct ttcctaccgc 1020
ccctcagata atgtaagctc atccaccaag aagcctgcac catgttttga ggttgagtga 1080

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<210> 100
<211> 359
<212> PRT
<213> Homo sapiens
<400> 100

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Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp
1          5          10          15
Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro
20        25        30
Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu
35        40        45
Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser
50        55        60
Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr
65        70        75        80
Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe
85        90        95
Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu
100       105       110
Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu
115       120       125
Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val
130       135       140
Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser
145       150       155       160

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Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn  
165 170 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro  
180 185 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe  
195 200 205

Leu Ile Ile Leu Thr Ser Tyr Phe Gly Ile Arg Lys His Leu Leu Lys  
210 215 220

Thr Asn Ser Tyr Gly Lys Asn Arg Ile Thr Arg Asp Gln Val Lys Lys  
225 230 235 240

Ile Ile Met Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Ile Pro His  
245 250 255

Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile Arg  
260 265 270

Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr Ile  
275 280 285

Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly Phe  
290 295 300

Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr Ile  
305 310 315 320

Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser Thr  
325 330 335

Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys Pro  
340 345 350

Ala Pro Cys Phe Glu Val Glu  
355

<210> 101  
<211> 37  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 101  
tccgaattcc aaaataactt gtaagaatga tcagaaa

37

<210> 102  
<211> 33  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 102  
agatcttaag aagataatta tggcaattgt gct

33

<210> 103

<211> 62  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Novel Sequence

<400> 103  
 aattcgaaaa cacttactga agacgaatag ctatgggaag aacaggataa cccgtgacca 60  
 ag 62

<210> 104  
 <211> 62  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Novel Sequence

<400> 104  
 ttaacttggt cacgggttat cctgttcttc ccatagctat tcgtcttcag taagtgtttt 60  
 cg 62

<210> 105  
 <211> 1083  
 <212> DNA  
 <213> Homo sapiens

<400> 105  
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 gctggaaggc ataattacat atttgtcatg attcctactt tatacagtat catctttgtg 120  
 gtgggaatat ttggaaacag cttgggtggtg atagtcattt acttttatat gaagctgaag 180  
 actgtggcca gtgtttttct tttgaattta gcaactggctg acttatgctt tttactgact 240  
 ttgccactat gggctgtcta cacagctatg gaataccgct ggccctttgg caattaccta 300  
 tgtaagattg cttcagccag cgtcagtttc aacctgtacg ctagtgtgtt tctactcacg 360  
 tgtctcagca ttgatcgata cctggctatt gttcacccaa tgaagtcccg ccttcgacgc 420  
 acaatgcttg tagccaaagt cacctgcatc atcatttggc tgctggcagg cttggccagt 480  
 ttgccagcta taatccatcg aaatgtattt ttcattgaga acaccaatat tacagtttgt 540  
 gctttccatt atgagtccca aaattcaacc cttccgatag ggctgggcct gacaaaaaat 600  
 atactggggtt tcctgtttcc ttttctgac atctttacaa gttatactct tatttggaag 660  
 gccctaaaga aggcttatga aattcagaag aacaaaccaa gaaatgatga tatttttaag 720  
 ataattatgg cagcaattgt gcttttcttt ttcttttcct ggattcccca ccaaatattc 780  
 acttttctgg atgtattgat tcaactaggc atcatagctg actgtagaat tgcagatatt 840  
 gtggacacgg ccatgcctat caccatttgt atagcttatt ttaacaattg cctgaatcct 900  
 cttttttatg gctttctggg gaaaaaattt aaaagatatt ttctccagct tctaaaatat 960

attcccccaa aagccaaatc ccactcaaac ctttcaacaa aaatgagcac gctttcctac 1020

cgcccctcag ataatgtaag ctcattccacc aagaagcctg caccatgttt tgaggttgag 1080

tga 1083

<210> 106

<211> 360

<212> PRT

<213> Homo sapiens

<400> 106

Met Ile Leu Asn Ser Ser Thr Glu Asp Gly Ile Lys Arg Ile Gln Asp  
1 5 10 15

Asp Cys Pro Lys Ala Gly Arg His Asn Tyr Ile Phe Val Met Ile Pro  
20 25 30

Thr Leu Tyr Ser Ile Ile Phe Val Val Gly Ile Phe Gly Asn Ser Leu  
35 40 45

Val Val Ile Val Ile Tyr Phe Tyr Met Lys Leu Lys Thr Val Ala Ser  
50 55 60

Val Phe Leu Leu Asn Leu Ala Leu Ala Asp Leu Cys Phe Leu Leu Thr  
65 70 75 80

Leu Pro Leu Trp Ala Val Tyr Thr Ala Met Glu Tyr Arg Trp Pro Phe  
85 90 95

Gly Asn Tyr Leu Cys Lys Ile Ala Ser Ala Ser Val Ser Phe Asn Leu  
100 105 110

Tyr Ala Ser Val Phe Leu Leu Thr Cys Leu Ser Ile Asp Arg Tyr Leu  
115 120 125

Ala Ile Val His Pro Met Lys Ser Arg Leu Arg Arg Thr Met Leu Val  
130 135 140

Ala Lys Val Thr Cys Ile Ile Ile Trp Leu Leu Ala Gly Leu Ala Ser  
145 150 155 160

Leu Pro Ala Ile Ile His Arg Asn Val Phe Phe Ile Glu Asn Thr Asn  
165 170 175

Ile Thr Val Cys Ala Phe His Tyr Glu Ser Gln Asn Ser Thr Leu Pro  
180 185 190

Ile Gly Leu Gly Leu Thr Lys Asn Ile Leu Gly Phe Leu Phe Pro Phe  
195 200 205

Leu Ile Ile Leu Thr Ser Tyr Thr Leu Ile Trp Lys Ala Leu Lys Lys  
210 215 220

Ala Tyr Glu Ile Gln Lys Asn Lys Pro Arg Asn Asp Asp Ile Phe Lys  
225 230 235 240

Ile Ile Met Ala Ala Ile Val Leu Phe Phe Phe Phe Ser Trp Ile Pro  
245 250 255

His Gln Ile Phe Thr Phe Leu Asp Val Leu Ile Gln Leu Gly Ile Ile  
260 265 270

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Arg Asp Cys Arg Ile Ala Asp Ile Val Asp Thr Ala Met Pro Ile Thr  
275 280 285

Ile Cys Ile Ala Tyr Phe Asn Asn Cys Leu Asn Pro Leu Phe Tyr Gly  
290 295 300

Phe Leu Gly Lys Lys Phe Lys Arg Tyr Phe Leu Gln Leu Leu Lys Tyr  
305 310 315 320

Ile Pro Pro Lys Ala Lys Ser His Ser Asn Leu Ser Thr Lys Met Ser  
325 330 335

Thr Leu Ser Tyr Arg Pro Ser Asp Asn Val Ser Ser Ser Thr Lys Lys  
340 345 350

Pro Ala Pro Cys Phe Glu Val Glu  
355 360

<210> 107  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 107  
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26

<210> 108  
<211> 38  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 108  
aagcacaatt gctgcataat tatcttaaaa atatcatc

38

<210> 109  
<211> 39  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 109  
aagataatta tggcagcaat tgtgcttttc tttttcttt

39

<210> 110  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 110  
gttgatcca cataatgcat tttctc

26



<210> 111  
 <211> 1344  
 <212> DNA  
 <213> Homo sapiens

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 ctgtgccgcc cgggggcgcc tctcctcaac agcagcagtg tgggcaacct cagctgcgag 120  
 cccctcgca ttcgcggagc cgggacacga gaattggagc tggccattag aatcactctt 180  
 tacgcagtga tcttctgat gagcgttgga ggaaatatgc tcatcatcgt ggtcctggga 240  
 ctgagccgcc gcctgaggac tgtcaccaat gccttctctc tctcactggc agtcagcgac 300  
 ctctgctgg ctgtggcttg catgcccttc accctctctc ccaatctcat gggcacattc 360  
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 tccacgctaa gcctcgtggc catcgcaactg gagcgatata gcgccatctg ccgaccactg 480  
 caggcacgag tgtggcagac gcgctccac gcgctcgcg tgattgtagc cagtggtgctg 540  
 ctgtccggac tactcatggt gccctacccc gtgtacactg tcgtgcaacc agtggggcct 600  
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 ctgctgcttc tgctcttgtt cttcatccca ggtgtgggta tggcgtggc ctacgggctt 720  
 atctctcgcg agctctactt agggcttcgc tttgacggcg acagtgcag cgacagccaa 780  
 agcaggggtcc gaaaccaagg cgggctgcca ggggctgttc accagaacgg gcgttgccgg 840  
 cctgagactg gcgcggttg caaagacagc gatggctgct acgtgcaact tccacgttcc 900  
 cggcctgccc tggagctgac ggcgctgacg gctcctgggc cgggatccgg ctcccggccc 960  
 acccaggcca agctgctggc taagaagcgc gtgaaacgaa tgttgctggt gatcgttgtg 1020  
 cttttttttc tgtgttggtt gccagtttat agtgccaaca cgtggcgcg ctttgatggc 1080  
 ccgggtgcac accgagcact ctcggtgct cctatctct tcatcactt gctgagctac 1140  
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 tgcttgaaaa cttgcgctcg ctgctgcccc cggcctccac gagctcgccc cagggtcttt 1260  
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 atcagcacac tgggccctgg ctga 1344

<210> 112  
 <211> 447  
 <212> PRT  
 <213> Homo sapiens

<400> 112

Met Glu Leu Leu Lys Leu Asn Arg Ser Val Gln Gly Thr Gly Pro Gly  
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Pro Gly Ala Ser Leu Cys Arg Pro Gly Ala Pro Leu Leu Asn Ser Ser

20                      25                      30  
 Ser Val Gly Asn Leu Ser Cys Glu Pro Pro Arg Ile Arg Gly Ala Gly  
       35                      40                      45  
 Thr Arg Glu Leu Glu Leu Ala Ile Arg Ile Thr Leu Tyr Ala Val Ile  
       50                      55                      60  
 Phe Leu Met Ser Val Gly Gly Asn Met Leu Ile Ile Val Val Leu Gly  
       65                      70                      75                      80  
 Leu Ser Arg Arg Leu Arg Thr Val Thr Asn Ala Phe Leu Leu Ser Leu  
               85                      90                      95  
 Ala Val Ser Asp Leu Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu  
               100                      105                      110  
 Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys  
               115                      120                      125  
 Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Ser Thr Leu Ser  
               130                      135                      140  
 Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu  
       145                      150                      155                      160  
 Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val  
               165                      170                      175  
 Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr  
               180                      185                      190  
 Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg  
               195                      200                      205  
 Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu  
               210                      215                      220  
 Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu  
       225                      230                      235                      240  
 Ile Ser Arg Glu Leu Tyr Leu Gly Leu Arg Phe Asp Gly Asp Ser Asp  
               245                      250                      255  
 Ser Asp Ser Gln Ser Arg Val Arg Asn Gln Gly Gly Leu Pro Gly Ala  
               260                      265                      270  
 Val His Gln Asn Gly Arg Cys Arg Pro Glu Thr Gly Ala Val Gly Lys  
               275                      280                      285  
 Asp Ser Asp Gly Cys Tyr Val Gln Leu Pro Arg Ser Arg Pro Ala Leu  
               290                      295                      300  
 Glu Leu Thr Ala Leu Thr Ala Pro Gly Pro Gly Ser Gly Ser Arg Pro  
       305                      310                      315                      320  
 Thr Gln Ala Lys Leu Leu Ala Lys Lys Arg Val Lys Arg Met Leu Leu  
               325                      330                      335  
 Val Ile Val Val Leu Phe Phe Leu Cys Trp Leu Pro Val Tyr Ser Ala  
               340                      345                      350  
 Asn Thr Trp Arg Ala Phe Asp Gly Pro Gly Ala His Arg Ala Leu Ser  
               355                      360                      365

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Val Ala Pro Ile Ser Phe Ile His Leu Leu Ser Tyr Ala Ser Ala Cys  
370 375 380

Val Asn Pro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala  
385 390 395 400

Cys Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg  
405 410 415

Pro Arg Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Ser Ile Ala Ser  
420 425 430

Leu Ser Arg Leu Ser Tyr Thr Thr Ile Ser Thr Leu Gly Pro Gly  
435 440 445

<210> 113  
<211> 34  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 113  
cagcagcatg cgcttcacgc gcttcttagc ccag

34

<210> 114  
<211> 35  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 114  
agaagcgcgt gaagcgcgtg ctgctggtga tcggt

35

<210> 115  
<211> 33  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 115  
atggagaaaa gaatcaaaag aatgttctat ata

33

<210> 116  
<211> 33  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 116  
tatatagaac attcttttga ttcttttctc cat

33

<210> 117  
<211> 30

<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 117  
cgctctctgg ccttgaagcg cacgctcagc

30

<210> 118  
<211> 30  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 118  
gctgagcgtg cgcttcaagg ccagagagcg

30

<210> 119  
<211> 30  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 119  
cccaggaaaa aggtgaaagt caaagttttc

30

<210> 120  
<211> 30  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 120  
gaaaactttg actttcacct ttttcctggg

30

<210> 121  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 121  
ggggcgcggg tgaaacggct ggtgagc

27

<210> 122  
<211> 27  
<212> DNA  
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<220>  
<223> Novel Sequence

<400> 122  
gctcaccagc cgtttcaccc gcgcccc 27

<210> 123  
<211> 30  
<212> DNA  
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<220>  
<223> Novel Sequence

<400> 123  
ccccttgaaa agcctaagaa cttggtcac 30

<210> 124  
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<212> DNA  
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<220>  
<223> Novel Sequence

<400> 124  
gatgaccaag ttcttaggct tttcaagggg 30

<210> 125  
<211> 32  
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<220>  
<223> Novel Sequence

<400> 125  
gatctctaga atgaacagca catgtattga ag 32

<210> 126  
<211> 35  
<212> DNA  
<213> Artificial

<220>  
<223> Novel Sequence

<400> 126  
ctagggtacc cgctcaagga cctctaattc catag 35

<210> 127  
<211> 1296  
<212> DNA  
<213> Homo sapiens

<400> 127  
atgcaggcgc ttaacattac cccggagcag ttctctcggc tgctgcggga ccacaacctg 60  
acgcgggagc agttcatcgc tctgtaccgg ctgcgaccgc tcgtctacac cccagagctg 120  
ccgggacgcg ccaagctggc cctcgtgctc accggcgtgc tcatcttcgc cctggcgctc 180

## Aren0054.ST25.txt

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tttggcaatg ctctggtggt ctacgtggtg acccgagca aggccatgc caccgtcacc 240
aacatcttta tctgctcctt ggcgctcagt gacctgtca tcaccttctt ctgcattccc 300
gtcaccatgc tccagaacat ttccgacaac tggctggggg gtgctttcat ttgcaagatg 360
gtgccatttg tccagtctac cgctgttggt acagaaatgc tcaactatgac ctgcattgct 420
gtggaaaggc accagggact tgtgcatcct tttaaaatga agtggcaata caccaaccga 480
agggctttca caatgctagg tgtggtctgg ctggtggcag tcatcgtagg atcacccatg 540
tggcacgtgc aacaacttga gatcaaatat gacttcctat atgaaaagga acacatctgc 600
tgcttagaag agtggaccag cctgtgcac cagaagatct acaccacctt catccttgtc 660
atcctcttcc tctgcctct tatggtgatg cttattctgt acagtaaaat tggttatgaa 720
ctttggataa agaaaagagt tggggatggt tcagtgttc gaactattca tggaaaagaa 780
atgtccaaaa tagccaggaa gaagaaacga gctaagatta tgatggtgac agtgggtggct 840
ctctttgctg tgtgctgggc accattccat gttgtccata tgatgattga atacagtaat 900
tttggaaagg aatatgatga tgtcacaatc aagatgattt ttgctatcgt gcaaattatt 960
ggattttcca actccatctg taatccatt gtctatgcat ttatgaatga aaacttcaaa 1020
aaaaatgttt tgtctgcagt ttgttattgc atagtaaata aaaccttctc tccagcacia 1080
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ctggctgaga attctccttt agacagtggg cattaa 1296

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<210> 128
<211> 431
<212> PRT
<213> Homo sapiens

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<400> 128

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Met Gln Ala Leu Asn Ile Thr Pro Glu Gln Phe Ser Arg Leu Leu Arg
1          5          10          15
Asp His Asn Leu Thr Arg Glu Gln Phe Ile Ala Leu Tyr Arg Leu Arg
20          25          30
Pro Leu Val Tyr Thr Pro Glu Leu Pro Gly Arg Ala Lys Leu Ala Leu
35          40          45
Val Leu Thr Gly Val Leu Ile Phe Ala Leu Ala Leu Phe Gly Asn Ala
50          55          60
Leu Val Phe Tyr Val Val Thr Arg Ser Lys Ala Met Arg Thr Val Thr
65          70          75          80
Asn Ile Phe Ile Cys Ser Leu Ala Leu Ser Asp Leu Leu Ile Thr Phe
85          90          95
Phe Cys Ile Pro Val Thr Met Leu Gln Asn Ile Ser Asp Asn Trp Leu

```

100

105

110

Gly Gly Ala Phe Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala  
115 120 125

Val Val Thr Glu Met Leu Thr Met Thr Cys Ile Ala Val Glu Arg His  
130 135 140

Gln Gly Leu Val His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg  
145 150 155 160

Arg Ala Phe Thr Met Leu Gly Val Val Trp Leu Val Ala Val Ile Val  
165 170 175

Gly Ser Pro Met Trp His Val Gln Gln Leu Glu Ile Lys Tyr Asp Phe  
180 185 190

Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp Thr Ser Pro  
195 200 205

Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile Leu Phe Leu  
210 215 220

Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile Gly Tyr Glu  
225 230 235 240

Leu Trp Ile Lys Lys Arg Val Gly Asp Gly Ser Val Leu Arg Thr Ile  
245 250 255

His Gly Lys Glu Met Ser Lys Ile Ala Arg Lys Lys Lys Arg Ala Lys  
260 265 270

Ile Met Met Val Thr Val Val Ala Leu Phe Ala Val Cys Trp Ala Pro  
275 280 285

Phe His Val Val His Met Met Ile Glu Tyr Ser Asn Phe Glu Lys Glu  
290 295 300

Tyr Asp Asp Val Thr Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile  
305 310 315 320

Gly Phe Ser Asn Ser Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn  
325 330 335

Glu Asn Phe Lys Lys Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val  
340 345 350

Asn Lys Thr Phe Ser Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr  
355 360 365

Met Met Arg Lys Lys Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu  
370 375 380

Glu Thr Lys Gly Glu Ala Phe Ser Asp Gly Asn Ile Glu Val Lys Leu  
385 390 395 400

Cys Glu Gln Thr Glu Glu Lys Lys Lys Leu Lys Arg His Leu Ala Leu  
405 410 415

Phe Arg Ser Glu Leu Ala Glu Asn Ser Pro Leu Asp Ser Gly His  
420 425 430

&lt;210&gt; 129

&lt;211&gt; 2040

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 129

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gcgctgccgc cttgcgaacga gcgccgtgc tcgccctttc ccctgggggc gctggtgccg	120
gtgaccgctg tgtgcctgtg cctgttcgtc gtcgggggtga gcggcaacgt ggtgaccgtg	180
atgctgatcg ggcgctaccg ggacatgcgg accaccacca acttgtacct gggcagcatg	240
gccgtgtccg acctactcat cctgctcggg ctgccgttcg acctgtaccg cctctggcgc	300
tcgcgccctt ggggtgttcg gccgctgctc tcgcgcctgt ccctctacct gggcgagggc	360
tgcacctacg ccacgctgct gcacatgacc gcgctcagcg tcgagcgcta cctggccatc	420
tgcgccccgc tccgcgcccg cgtcttggtc acccgggccc gcgtccgcgc gctcatcgct	480
gtgctctggg ccgtggcgct gctctctgcc ggtcccttct tgttcctggt gggcgtcgag	540
caggaccccg gcatctccgt agtcccgggc ctcaatggca ccgcgcggat cgcctcctcg	600
cctctgcctt cgtcgccgcc tctctggctc tcgcgggggc caccgcctc cccgccgtcg	660
gggcccagaa ccgcggaggc cgcgcgctg ttccagccgcg aatgccggcc gagccccgcg	720
cagctgggcg cgctgcgtgt catgctgtgg gtcaccaccg cctacttctt cctgcccttt	780
ctgtgcctca gcatcctcta cgggctcatc gggcgggagc tgtggagcag ccggcgggccg	840
ctgcgaggcc cgccgcctc gggcggggag agaggccacc ggcagaccaa acgcgtcctg	900
cgtaagtgga gccgcccgtg ttccaaagac gctgcctgc agtccgcccc gccggggacc	960
gcgcaaacgc tgggtcccct tcccctgctc gccagctctt gggcgccgct tccagctccc	1020
tttctatatt cgattccagc ctccaccgc cggtacttcc catccccga gaaaaccatg	1080
tcctgtcccc caggagctct gggggacccc agggcgcttt gaggtgaggc tcccggatc	1140
cgattcagta accagcagtg cttttccaga gcctctgaga ccagaaagga gagttggtaa	1200
ttcttaatcc aaccacctgt tagatgccac aaatgaggag tcctcacagt gctcttgaga	1260
agacgaggga gatttcatta agctaaaatt ttttatttaa tgtaagtga tgctgaaggc	1320
taaagtaaac cttgctcgta tcaaaaagta aagattgtgc agacctgtg tagaattctt	1380
ttcaacagag aacagaaaac ttgtctccga agtgggtttg tggaaggag cctgccaagg	1440
cggcttggtc agagaaattg ctcttctggt tttatgtoca gccttgataa cacatatggg	1500
agcctactat gcagttttaa agcaagtatc catgcagcct gcagcctggt cattttttct	1560
ggggtgagga tctgcctagg tagaagtttt ctctaattta ttttgcgtt acttggtatt	1620
gcagatggtt ccttgctcgg gtgggggggt tatttgcttc ccaatgcttt tgtaaatccc	1680
ggtgctgtgt cttatgttgc agtgggtgtg gttctggcat ttataatttg ctggttgccc	1740
ttccacgttg gcagaatcat ttacataaac acggaagatt cgcgatgat gtacttctct	1800
cagtacttta acatcgtcgc tctgcaactt ttctatctga gcgcatctat caaccaatc	1860



## Aren0054.ST25.txt

ctctacaacc tcatttcaaa gaagtacaga gcggcgccct ttaaactgct gctcgcaagg 1920  
 aagtcaggc cgagaggctt ccacagaagc agggacactg cgggggaagt tgcaggggac 1980  
 actggaggag acacggtggg ctacaccgag acaagcgcta acgtgaagac gatgggataa 2040

<210> 130  
 <211> 412  
 <212> PRT  
 <213> Homo sapiens

<400> 130

Met Gly Ser Pro Trp Asn Gly Ser Asp Gly Pro Glu Gly Ala Arg Glu  
 1 5 10 15  
 Pro Pro Trp Pro Ala Leu Pro Pro Cys Asp Glu Arg Arg Cys Ser Pro  
 20 25 30  
 Phe Pro Leu Gly Ala Leu Val Pro Val Thr Ala Val Cys Leu Cys Leu  
 35 40 45  
 Phe Val Val Gly Val Ser Gly Asn Val Val Thr Val Met Leu Ile Gly  
 50 55 60  
 Arg Tyr Arg Asp Met Arg Thr Thr Thr Asn Leu Tyr Leu Gly Ser Met  
 65 70 75 80  
 Ala Val Ser Asp Leu Leu Ile Leu Leu Gly Leu Pro Phe Asp Leu Tyr  
 85 90 95  
 Arg Leu Trp Arg Ser Arg Pro Trp Val Phe Gly Pro Leu Leu Cys Arg  
 100 105 110  
 Leu Ser Leu Tyr Val Gly Glu Gly Cys Thr Tyr Ala Thr Leu Leu His  
 115 120 125  
 Met Thr Ala Leu Ser Val Glu Arg Tyr Leu Ala Ile Cys Arg Pro Leu  
 130 135 140  
 Arg Ala Arg Val Leu Val Thr Arg Arg Arg Val Arg Ala Leu Ile Ala  
 145 150 155 160  
 Val Leu Trp Ala Val Ala Leu Leu Ser Ala Gly Pro Phe Leu Phe Leu  
 165 170 175  
 Val Gly Val Glu Gln Asp Pro Gly Ile Ser Val Val Pro Gly Leu Asn  
 180 185 190  
 Gly Thr Ala Arg Ile Ala Ser Ser Pro Leu Ala Ser Ser Pro Pro Leu  
 195 200 205  
 Trp Leu Ser Arg Ala Pro Pro Pro Ser Pro Pro Ser Gly Pro Glu Thr  
 210 215 220  
 Ala Glu Ala Ala Ala Leu Phe Ser Arg Glu Cys Arg Pro Ser Pro Ala  
 225 230 235 240  
 Gln Leu Gly Ala Leu Arg Val Met Leu Trp Val Thr Thr Ala Tyr Phe  
 245 250 255  
 Phe Leu Pro Phe Leu Cys Leu Ser Ile Leu Tyr Gly Leu Ile Gly Arg  
 260 265 270

## Aren0054.ST25.txt

Glu Leu Trp Ser Ser Arg Arg Pro Leu Arg Gly Pro Ala Ala Ser Gly  
275 280 285

Arg Glu Arg Gly His Arg Gln Thr Lys Arg Val Leu Leu Val Val Val  
290 295 300

Leu Ala Phe Ile Ile Cys Trp Leu Pro Phe His Val Gly Arg Ile Ile  
305 310 315 320

Tyr Ile Asn Thr Glu Asp Ser Arg Met Met Tyr Phe Ser Gln Tyr Phe  
325 330 335

Asn Ile Val Ala Leu Gln Leu Phe Tyr Leu Ser Ala Ser Ile Asn Pro  
340 345 350

Ile Leu Tyr Asn Leu Ile Ser Lys Lys Tyr Arg Ala Ala Ala Phe Lys  
355 360 365

Leu Leu Leu Ala Arg Lys Ser Arg Pro Arg Gly Phe His Arg Ser Arg  
370 375 380

Asp Thr Ala Gly Glu Val Ala Gly Asp Thr Gly Gly Asp Thr Val Gly  
385 390 395 400

Tyr Thr Glu Thr Ser Ala Asn Val Lys Thr Met Gly  
405 410

<210> 131  
<211> 1344  
<212> DNA  
<213> Homo sapiens

<400> 131  
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ctgtgccgcc cgggggccc tctcctcaac agcagcagtg tgggcaacct cagctgcgag 120  
ccccctcgca ttcgcggagc cgggacacga gaattggagc tggccattag aatcactctt 180  
tacgcagtgat tcttctgat gagcgttgga ggaaatatgc tcatcatcgt ggtcctggga 240  
ctgagccgcc gcctgaggac tgtcaccaat gccttctctc tctcactggc agtcagcgac 300  
ctcctgctgg ctgtggcttg catgcccttc accctcctgc ccaatctcat gggcacattc 360  
atctttggca cgtcatctg caaggcgggt tctacacctc tgggggtgtc tgtgagtgtg 420  
tccacgctaa gcctcgtggc catcgactg gagcgatata gcgccatctg ccgaccactg 480  
caggcacgag tgtggcagac gcgctccac gcggctcgcg tgattgtagc cacgtggctg 540  
ctgtccggac tactcatggt gccctacccc gtgtacactg tcgtgcaacc agtggggcct 600  
cgtgtgctgc agtgctgca tcgtggccc agtgcgcggg tccgccagac ctggtccgta 660  
ctgtgcttc tgctcttgtt cttcatccca ggtgtgggta tggccgtggc ctacgggctt 720  
atctctcgcg agctctactt agggcttcgc tttagcggcg acagtgcagc cgacagccaa 780  
agcagggtcc gaaaccaagg cgggctgcca ggggctgttc accagaacgg gcgttgccgg 840  
cctgagactg gcgcggttg caaagacagc gatggctgct acgtgcaact tccacgttcc 900  
cggcctgccc tggagctgac ggcgctgacg gctcctgggc cgggatccgg ctcccggccc 960

## Aren0054.ST25.txt

acccaggcca agctgctggc taagaagcgc gtgaaacgaa tggtgctggt gatcgttggtg 1020  
 ctttttttttc tgtgttggtt gccagtttat agtgccaaca cgtggcgcg ctttgatggc 1080  
 ccgggtgcac accgagcact ctccgggtgct cctatctcct tcattcactt gctgagctac 1140  
 gcctcggcct gtgtcaaccc cctggtctac tgcttcatgc accgtcgctt tcgccaggcc 1200  
 tgcttggaac cttgcgctcg ctgctgcccc cgccctccac gagctcgccc cagggtcttt 1260  
 cccgatgagg accctccac tcctccatt gcttcgctgt ccaggcttag ctacaccacc 1320  
 atcagcacac tgggccctgg ctga 1344

<210> 132  
 <211> 447  
 <212> PRT  
 <213> Homo sapiens

<400> 132

Met Glu Leu Leu Lys Leu Asn Arg Ser Val Gln Gly Thr Gly Pro Gly  
 1 5 10 15  
 Pro Gly Ala Ser Leu Cys Arg Pro Gly Ala Pro Leu Leu Asn Ser Ser  
 20 25 30  
 Ser Val Gly Asn Leu Ser Cys Glu Pro Pro Arg Ile Arg Gly Ala Gly  
 35 40 45  
 Thr Arg Glu Leu Glu Leu Ala Ile Arg Ile Thr Leu Tyr Ala Val Ile  
 50 55 60  
 Phe Leu Met Ser Val Gly Gly Asn Met Leu Ile Ile Val Val Leu Gly  
 65 70 75 80  
 Leu Ser Arg Arg Leu Arg Thr Val Thr Asn Ala Phe Leu Leu Ser Leu  
 85 90 95  
 Ala Val Ser Asp Leu Leu Leu Ala Val Ala Cys Met Pro Phe Thr Leu  
 100 105 110  
 Leu Pro Asn Leu Met Gly Thr Phe Ile Phe Gly Thr Val Ile Cys Lys  
 115 120 125  
 Ala Val Ser Tyr Leu Met Gly Val Ser Val Ser Val Ser Thr Leu Ser  
 130 135 140  
 Leu Val Ala Ile Ala Leu Glu Arg Tyr Ser Ala Ile Cys Arg Pro Leu  
 145 150 155 160  
 Gln Ala Arg Val Trp Gln Thr Arg Ser His Ala Ala Arg Val Ile Val  
 165 170 175  
 Ala Thr Trp Leu Leu Ser Gly Leu Leu Met Val Pro Tyr Pro Val Tyr  
 180 185 190  
 Thr Val Val Gln Pro Val Gly Pro Arg Val Leu Gln Cys Val His Arg  
 195 200 205  
 Trp Pro Ser Ala Arg Val Arg Gln Thr Trp Ser Val Leu Leu Leu Leu  
 210 215 220  
 Leu Leu Phe Phe Ile Pro Gly Val Val Met Ala Val Ala Tyr Gly Leu

[illegible]

## Aren0054.ST25.txt

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atcaacctca acttggtcag gacgtgtaca ggctatgcaa tacctttggt caccatcctg 600
atctgtaacc ggaaagtcta ccaagctgtg cggcacaata aagccacgga aaacaaggaa 660
aagaagagaa tcaaaaaact acttgtcagc atcacagtta cttttgtcct atgctttact 720
ccctttcatg tgatgttgct gattcgtgc attttagagc atgctgtgaa cttcgaagac 780
cacagcaatt ctgggaagcg aacttacaca atgtatagaa tcacgggtgc attaacaagt 840
ttaaattgtg ttgctgatcc aattctgtac tgttttgta ccgaaacagg aagatatgat 900
atgtggaata tattaaaatt ctgcactggg aggtgtaata catcaciaag acaaagaaaa 960
cgcatacttt ctgtgtctac aaaagatact atggaattag aggtccttga gtag 1014

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<210> 134  
 <211> 337  
 <212> PRT  
 <213> Homo sapiens

<400> 134

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Met Asn Ser Thr Cys Ile Glu Glu Gln His Asp Leu Asp His Tyr Leu
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Phe Pro Ile Val Tyr Ile Phe Val Ile Ile Val Ser Ile Pro Ala Asn
20        25        30
Ile Gly Ser Leu Cys Val Ser Phe Leu Gln Ala Lys Lys Glu Ser Glu
35        40        45
Leu Gly Ile Tyr Leu Phe Ser Leu Ser Leu Ser Asp Leu Leu Tyr Ala
50        55        60
Leu Thr Leu Pro Leu Trp Ile Asp Tyr Thr Trp Asn Lys Asp Asn Trp
65        70        75        80
Thr Phe Ser Pro Ala Leu Cys Lys Gly Ser Ala Phe Leu Met Tyr Met
85        90        95
Asn Phe Tyr Ser Ser Thr Ala Phe Leu Thr Cys Ile Ala Val Asp Arg
100       105       110
Tyr Leu Ala Val Val Tyr Pro Leu Lys Phe Phe Phe Leu Arg Thr Arg
115       120       125
Arg Phe Ala Leu Met Val Ser Leu Ser Ile Trp Ile Leu Glu Thr Ile
130       135       140
Phe Asn Ala Val Met Leu Trp Glu Asp Glu Thr Val Val Glu Tyr Cys
145       150       155       160
Asp Ala Glu Lys Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr Pro Leu
165       170       175
Glu Lys Trp Gln Ile Asn Leu Asn Leu Phe Arg Thr Cys Thr Gly Tyr
180       185       190
Ala Ile Pro Leu Val Thr Ile Leu Ile Cys Asn Arg Lys Val Tyr Gln
195       200       205
Ala Val Arg His Asn Lys Ala Thr Glu Asn Lys Glu Lys Lys Arg Ile
210       215       220

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Aren0054.ST25.txt

Lys Lys Leu Leu Val Ser Ile Thr Val Thr Phe Val Leu Cys Phe Thr  
 225 230 235 240  
 Pro Phe His Val Met Leu Leu Ile Arg Cys Ile Leu Glu His Ala Val  
 245 250 255  
 Asn Phe Glu Asp His Ser Asn Ser Gly Lys Arg Thr Tyr Thr Met Tyr  
 260 265 270  
 Arg Ile Thr Val Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile  
 275 280 285  
 Leu Tyr Cys Phe Val Thr Glu Thr Gly Arg Tyr Asp Met Trp Asn Ile  
 290 295 300  
 Leu Lys Phe Cys Thr Gly Arg Cys Asn Thr Ser Gln Arg Gln Arg Lys  
 305 310 315 320  
 Arg Ile Leu Ser Val Ser Thr Lys Asp Thr Met Glu Leu Glu Val Leu  
 325 330 335

Glu

<210> 135  
 <211> 999  
 <212> DNA  
 <213> Homo sapiens

<400> 135  
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 tacagactgc acagcaatgc cagtgaagtc cttggaaaag gctactctga tggagggtgc 120  
 tacgagcaac tttttgtctc tctgaggtg tttgtgactc tgggtgtcat cagcttgttg 180  
 gagaatatct tagtgattgt ggcaatagcc aagaacaaga atctgcattc acccatgtac 240  
 tttttcatct gcagcttggc tgtggctgat atgctggtga gcgtttcaaa tggatcagaa 300  
 accattatca tcacctatt aaacagtaca gatacggatg cacagagttt cacagtgaat 360  
 attgataatg tcattgactc ggtgatctgt agtccttgc ttgcatccat ttgcagcctg 420  
 ctttcaattg cagtggacag gtactttact atcttctatg ctctccagta ccataacatt 480  
 atgacagtta agcgggttgg gatcagcata agttgtatct gggcagcttg cacggtttca 540  
 ggcattttgt tcatcattta ctcatagatg agtgctgtca tcatctgcct catcaccatg 600  
 ttcttcacca tgctggctct catggcttct ctctatgtcc acatgttctt gatggccagg 660  
 cttcacatta agaggattgc tgtcctcccc ggcactgggtg ccatccgcca aggtgccaat 720  
 atgaaggaa aaattacctt gaccatcctg attggcgtct ttgttgtctg ctgggcccga 780  
 ttcttctctc acttaatat ctacatctct tgtcctcaga atccatattg tgtgtgcttc 840  
 atgtctcact ttaacttgta tctcatactg atcatgtgta attcaatcat cgatcctctg 900  
 atttatgcac tccggagtca agaactgagg aaaaccttca aagagatcat ctgttgctat 960  
 cccctgggag gcctttgtga cttgtctagc agatattaa 999

<210> 136  
 <211> 332  
 <212> PRT  
 <213> Homo sapiens

<400> 136

Met Val Asn Ser Thr His Arg Gly Met His Thr Ser Leu His Leu Trp  
 1 5 10 15

Asn Arg Ser Ser Tyr Arg Leu His Ser Asn Ala Ser Glu Ser Leu Gly  
 20 25 30

Lys Gly Tyr Ser Asp Gly Gly Cys Tyr Glu Gln Leu Phe Val Ser Pro  
 35 40 45

Glu Val Phe Val Thr Leu Gly Val Ile Ser Leu Leu Glu Asn Ile Leu  
 50 55 60

Val Ile Val Ala Ile Ala Lys Asn Lys Asn Leu His Ser Pro Met Tyr  
 65 70 75 80

Phe Phe Ile Cys Ser Leu Ala Val Ala Asp Met Leu Val Ser Val Ser  
 85 90 95

Asn Gly Ser Glu Thr Ile Ile Ile Thr Leu Leu Asn Ser Thr Asp Thr  
 100 105 110

Asp Ala Gln Ser Phe Thr Val Asn Ile Asp Asn Val Ile Asp Ser Val  
 115 120 125

Ile Cys Ser Ser Leu Leu Ala Ser Ile Cys Ser Leu Leu Ser Ile Ala  
 130 135 140

Val Asp Arg Tyr Phe Thr Ile Phe Tyr Ala Leu Gln Tyr His Asn Ile  
 145 150 155 160

Met Thr Val Lys Arg Val Gly Ile Ser Ile Ser Cys Ile Trp Ala Ala  
 165 170 175

Cys Thr Val Ser Gly Ile Leu Phe Ile Ile Tyr Ser Asp Ser Ser Ala  
 180 185 190

Val Ile Ile Cys Leu Ile Thr Met Phe Phe Thr Met Leu Ala Leu Met  
 195 200 205

Ala Ser Leu Tyr Val His Met Phe Leu Met Ala Arg Leu His Ile Lys  
 210 215 220

Arg Ile Ala Val Leu Pro Gly Thr Gly Ala Ile Arg Gln Gly Ala Asn  
 225 230 235 240

Met Lys Gly Lys Ile Thr Leu Thr Ile Leu Ile Gly Val Phe Val Val  
 245 250 255

Cys Trp Ala Pro Phe Phe Leu His Leu Ile Phe Tyr Ile Ser Cys Pro  
 260 265 270

Gln Asn Pro Tyr Cys Val Cys Phe Met Ser His Phe Asn Leu Tyr Leu  
 275 280 285

Ile Leu Ile Met Cys Asn Ser Ile Ile Asp Pro Leu Ile Tyr Ala Leu  
 290 295 300

## Aren0054.ST25.txt

Arg Ser Gln Glu Leu Arg Lys Thr Phe Lys Glu Ile Ile Cys Cys Tyr  
 305 310 315 320

Pro Leu Gly Gly Leu Cys Asp Leu Ser Ser Arg Tyr  
 325 330

<210> 137  
 <211> 33  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Novel Sequence

<400> 137  
 gccaatatga agggaaaaat taccttgacc atc 33

<210> 138  
 <211> 31  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Novel Sequence

<400> 138  
 ctccttcggt cctcctatcg ttgtcagaag t 31

<210> 139  
 <211> 1842  
 <212> DNA  
 <213> Homo sapiens

<400> 139  
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 ccagaatacc caccggctct aatcatcttt atgttctgcg cgatggttat caccatcggt 120  
 gtagacctaa tcggcaactc catggtcatt ttggctgtga cgaagaacaa gaagctccgg 180  
 aattctggca acatcttcgt ggtcagtctc tctgtggccg atatgctggt ggccatctac 240  
 ccataccctt tgatgctgca tgccatgtcc attgggggct gggatctgag ccagttacag 300  
 tgccagatgg tcgggttcat cacagggctg agtgtggtcg gctccatctt caacatcgtg 360  
 gcaatcgcta tcaaccgtta ctgctacatc tgccacagcc tccagtacga acggatcttc 420  
 agtgtgcgca atacctgcat ctacctgggtc atcacctgga tcatgaccgt cctggctgtc 480  
 ctgccaaca tgtacattgg caccatcgag tacgatctc gcacctacac ctgcatcttc 540  
 aactatctga acaaccctgt cttcactgtt accatcgtct gcatccactt cgtcctccct 600  
 ctctcatcg tgggtttctg ctacgtgagg atctggacca aagtgtggc ggcccgtgac 660  
 cctgcagggc agaatcctga caaccaactt gctgaggttc gcaattttct aaccatgttt 720  
 gtgatcttcc tcctctttgc agtgtgctgg tgccctatca acgtgctcac tgtcttggtg 780  
 gctgtcagtc cgaaggagat ggcaggcaag atccccaact ggctttatct tgcagcctac 840  
 ttcatagcct acttcaacag ctgcctcaac gctgtgatct acgggctcct caatgagaat 900



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ttccgaagag aatactggac catcttccat gctatgcggc accctatcat attcttcct 960
ggcctcatca gtgatattcg tgagatgcag gaggcccgta ccctggcccg cgcccgaggc 1020
catgctcgcg accaagctcg tgaacaagac cgtgcccag cctgtcctgc tgtggaggaa 1080
accccgatga atgtccggaa tgttccatta cctggatgat ctgcagctgg ccaccccgac 1140
cgtgcctctg gccaccctaa gccccattcc agatcctcct ctgcctatcg caaatctgcc 1200
tctaccacc acaagtctgt ctttagccac tccaaggctg cctctggta cctcaagcct 1260
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aagcctgact ctgttcattt caagcctgct tccagcaacc ccaagcccat cactggccac 1440
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cccgagatcc ctgccattgc ccaccctgtg tctgacgaca gtgacctccc tgagtcggcc 1680
tctagccctg ccgctggggc caccaagcct gctgccagcc agctggagtc tgacaccatc 1740
gctgaccttc ctgaccttac tgtagtcaat accagtacca atgattacca tgatgtcgtg 1800
gttgttgatg ttgaagatga tcctgatgaa atggctgtgt ga 1842

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<210> 140
<211> 613
<212> PRT
<213> Homo sapiens

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<400> 140

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Met Gly Pro Thr Leu Ala Val Pro Thr Pro Tyr Gly Cys Ile Gly Cys
1          5          10          15
Lys Leu Pro Gln Pro Glu Tyr Pro Pro Ala Leu Ile Ile Phe Met Phe
20          25          30
Cys Ala Met Val Ile Thr Ile Val Val Asp Leu Ile Gly Asn Ser Met
35          40          45
Val Ile Leu Ala Val Thr Lys Asn Lys Lys Leu Arg Asn Ser Gly Asn
50          55          60
Ile Phe Val Val Ser Leu Ser Val Ala Asp Met Leu Val Ala Ile Tyr
65          70          75          80
Pro Tyr Pro Leu Met Leu His Ala Met Ser Ile Gly Gly Trp Asp Leu
85          90          95
Ser Gln Leu Gln Cys Gln Met Val Gly Phe Ile Thr Gly Leu Ser Val
100         105         110
Val Gly Ser Ile Phe Asn Ile Val Ala Ile Ala Ile Asn Arg Tyr Cys
115         120         125

```

## Aren0054.ST25.txt

Tyr Ile Cys His Ser Leu Gln Tyr Glu Arg Ile Phe Ser Val Arg Asn  
 130 135 140  
 Thr Cys Ile Tyr Leu Val Ile Thr Trp Ile Met Thr Val Leu Ala Val  
 145 150 155 160  
 Leu Pro Asn Met Tyr Ile Gly Thr Ile Glu Tyr Asp Pro Arg Thr Tyr  
 165 170 175  
 Thr Cys Ile Phe Asn Tyr Leu Asn Asn Pro Val Phe Thr Val Thr Ile  
 180 185 190  
 Val Cys Ile His Phe Val Leu Pro Leu Leu Ile Val Gly Phe Cys Tyr  
 195 200 205  
 Val Arg Ile Trp Thr Lys Val Leu Ala Ala Arg Asp Pro Ala Gly Gln  
 210 215 220  
 Asn Pro Asp Asn Gln Leu Ala Glu Val Arg Asn Phe Leu Thr Met Phe  
 225 230 235 240  
 Val Ile Phe Leu Leu Phe Ala Val Cys Trp Cys Pro Ile Asn Val Leu  
 245 250 255  
 Thr Val Leu Val Ala Val Ser Pro Lys Glu Met Ala Gly Lys Ile Pro  
 260 265 270  
 Asn Trp Leu Tyr Leu Ala Ala Tyr Phe Ile Ala Tyr Phe Asn Ser Cys  
 275 280 285  
 Leu Asn Ala Val Ile Tyr Gly Leu Leu Asn Glu Asn Phe Arg Arg Glu  
 290 295 300  
 Tyr Trp Thr Ile Phe His Ala Met Arg His Pro Ile Ile Phe Phe Pro  
 305 310 315 320  
 Gly Leu Ile Ser Asp Ile Arg Glu Met Gln Glu Ala Arg Thr Leu Ala  
 325 330 335  
 Arg Ala Arg Ala His Ala Arg Asp Gln Ala Arg Glu Gln Asp Arg Ala  
 340 345 350  
 His Ala Cys Pro Ala Val Glu Glu Thr Pro Met Asn Val Arg Asn Val  
 355 360 365  
 Pro Leu Pro Gly Asp Ala Ala Ala Gly His Pro Asp Arg Ala Ser Gly  
 370 375 380  
 His Pro Lys Pro His Ser Arg Ser Ser Ser Ala Tyr Arg Lys Ser Ala  
 385 390 395 400  
 Ser Thr His His Lys Ser Val Phe Ser His Ser Lys Ala Ala Ser Gly  
 405 410 415  
 His Leu Lys Pro Val Ser Gly His Ser Lys Pro Ala Ser Gly His Pro  
 420 425 430  
 Lys Ser Ala Thr Val Tyr Pro Lys Pro Ala Ser Val His Phe Lys Gly  
 435 440 445  
 Asp Ser Val His Phe Lys Gly Asp Ser Val His Phe Lys Pro Asp Ser  
 450 455 460  
 Val His Phe Lys Pro Ala Ser Ser Asn Pro Lys Pro Ile Thr Gly His  
 465 470 475 480

His Val Ser Ala Gly Ser His Ser Lys Ser Ala Phe Ser Ala Ala Thr  
 485 490 495

Ser His Pro Lys Pro Ile Lys Pro Ala Thr Ser His Ala Glu Pro Thr  
 500 505 510

Thr Ala Asp Tyr Pro Lys Pro Ala Thr Thr Ser His Pro Lys Pro Ala  
 515 520 525

Ala Ala Asp Asn Pro Glu Leu Ser Ala Ser His Cys Pro Glu Ile Pro  
 530 535 540

Ala Ile Ala His Pro Val Ser Asp Asp Ser Asp Leu Pro Glu Ser Ala  
 545 550 555 560

Ser Ser Pro Ala Ala Gly Pro Thr Lys Pro Ala Ala Ser Gln Leu Glu  
 565 570 575

Ser Asp Thr Ile Ala Asp Leu Pro Asp Pro Thr Val Val Thr Thr Ser  
 580 585 590

Thr Asn Asp Tyr His Asp Val Val Val Val Asp Val Glu Asp Asp Pro  
 595 600 605

Asp Glu Met Ala Val  
 610

<210> 141  
 <211> 1842  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
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 ccagaatacc caccggctct aatcatcttt atgttctgcg cgatgggtat caccatcggt 120  
 gtagacctaa tcggcaactc catggtcatt ttggctgta cgaagaacaa gaagctccgg 180  
 aattctggca acatcttcgt ggtcagtcct tctgtggccg atatgctggg ggccatctac 240  
 ccataccctt tgatgctgca tgccatgtcc attgggggct gggatctgag ccagttacag 300  
 tgccagatgg tcgggttcat cacagggtcg agtgtggtcg gctccatctt caacatcggt 360  
 gcaatcgcta tcaaccgtta ctgtacatc tgccacagcc tccagtacga acggatcttc 420  
 agtgtgcgca atacctgcat ctacctggtc atcacctgga tcatgaccgt cctggctgtc 480  
 ctgcccacaa tgtacattgg caccatcgag tacgatcctc gcacctacac ctgcatcttc 540  
 aactatctga acaaccctgt cttactggt accatcgctt gcatccactt cgtcctccct 600  
 ctctcatcg tgggtttctg ctacgtgagg atctggacca aagtgtggc ggcccgtagc 660  
 cctgcagggc agaatcctga caaccaactt gctgagggtc gcaataaact aaccatgttt 720  
 gtgatcttcc tcctctttgc agtgtgctgg tgccctatca acgtgctcac tgtcttggtg 780  
 gctgtcagtc cgaaggagat ggcaggcaag atccccaact ggctttatct tgcagcctac 840  
 ttcatagcct acttcaacag ctgcctcaac gctgtgatct acgggctcct caatgagaat 900  
 ttccgaagag aatactggac catcttccat gctatgcggc accctatcat attcttctct 960

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ggcctcatca gtgatattcg tgagatgcag gagggccgta ccctggcccg cgcccgtgcc 1020
catgctcgcg accaagctcg tgaacaagac cgtgcccatg cctgtcctgc tgtggaggaa 1080
accccgatga atgtccggaa tgttccatta cctggtgatg ctgcagctgg ccaccccgac 1140
cgtgcctctg gccaccctaa gcccattcc agatcctcct ctgcctatcg caaatctgcc 1200
tctaccacc acaagtctgt ctttagccac tccaaggctg cctctggtca cctcaagcct 1260
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aagcctgact ctgttcattt caagcctgct tccagcaacc ccaagcccat cactggccac 1440
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cccatcaagc cagctaccag ccattgctgag cccaccactg ctgactatcc caagcctgcc 1560
actaccagcc accctaagcc cgctgctgct gacaaccctg agctctctgc ctcccattgc 1620
cccgagatcc ctgccattgc ccaccctgtg tctgacgaca gtgacctccc tgagtcggcc 1680
tctagccctg ccgctggggc caccaagcct gctgccagcc agctggagtc tgacaccatc 1740
gctgaccttc ctgaccctac tgtagtcact accagtacca atgattacca tgatgtcgtg 1800
gttgttgatg ttgaagatga tcctgatgaa atggctgtgt ga 1842

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<210> 142
<211> 613
<212> PRT
<213> Homo sapiens

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<400> 142

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Met Gly Pro Thr Leu Ala Val Pro Thr Pro Tyr Gly Cys Ile Gly Cys
1          5          10          15
Lys Leu Pro Gln Pro Glu Tyr Pro Pro Ala Leu Ile Ile Phe Met Phe
20        25        30
Cys Ala Met Val Ile Thr Ile Val Val Asp Leu Ile Gly Asn Ser Met
35        40        45
Val Ile Leu Ala Val Thr Lys Asn Lys Lys Leu Arg Asn Ser Gly Asn
50        55        60
Ile Phe Val Val Ser Leu Ser Val Ala Asp Met Leu Val Ala Ile Tyr
65        70        75        80
Pro Tyr Pro Leu Met Leu His Ala Met Ser Ile Gly Gly Trp Asp Leu
85        90        95
Ser Gln Leu Gln Cys Gln Met Val Gly Phe Ile Thr Gly Leu Ser Val
100       105       110
Val Gly Ser Ile Phe Asn Ile Val Ala Ile Ala Ile Asn Arg Tyr Cys
115       120       125
Tyr Ile Cys His Ser Leu Gln Tyr Glu Arg Ile Phe Ser Val Arg Asn
130       135       140

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## Aren0054.ST25.txt

Thr Cys Ile Tyr Leu Val Ile Thr Trp Ile Met Thr Val Leu Ala Val  
 145 150 155 160  
 Leu Pro Asn Met Tyr Ile Gly Thr Ile Glu Tyr Asp Pro Arg Thr Tyr  
 165 170 175  
 Thr Cys Ile Phe Asn Tyr Leu Asn Asn Pro Val Phe Thr Val Thr Ile  
 180 185 190  
 Val Cys Ile His Phe Val Leu Pro Leu Leu Ile Val Gly Phe Cys Tyr  
 195 200 205  
 Val Arg Ile Trp Thr Lys Val Leu Ala Ala Arg Asp Pro Ala Gly Gln  
 210 215 220  
 Asn Pro Asp Asn Gln Leu Ala Glu Val Arg Asn Lys Leu Thr Met Phe  
 225 230 235 240  
 Val Ile Phe Leu Leu Phe Ala Val Cys Trp Cys Pro Ile Asn Val Leu  
 245 250 255  
 Thr Val Leu Val Ala Val Ser Pro Lys Glu Met Ala Gly Lys Ile Pro  
 260 265 270  
 Asn Trp Leu Tyr Leu Ala Ala Tyr Phe Ile Ala Tyr Phe Asn Ser Cys  
 275 280 285  
 Leu Asn Ala Val Ile Tyr Gly Leu Leu Asn Glu Asn Phe Arg Arg Glu  
 290 295 300  
 Tyr Trp Thr Ile Phe His Ala Met Arg His Pro Ile Ile Phe Phe Ser  
 305 310 315 320  
 Gly Leu Ile Ser Asp Ile Arg Glu Met Gln Glu Ala Arg Thr Leu Ala  
 325 330 335  
 Arg Ala Arg Ala His Ala Arg Asp Gln Ala Arg Glu Gln Asp Arg Ala  
 340 345 350  
 His Ala Cys Pro Ala Val Glu Glu Thr Pro Met Asn Val Arg Asn Val  
 355 360 365  
 Pro Leu Pro Gly Asp Ala Ala Ala Gly His Pro Asp Arg Ala Ser Gly  
 370 375 380  
 His Pro Lys Pro His Ser Arg Ser Ser Ser Ala Tyr Arg Lys Ser Ala  
 385 390 395 400  
 Ser Thr His His Lys Ser Val Phe Ser His Ser Lys Ala Ala Ser Gly  
 405 410 415  
 His Leu Lys Pro Val Ser Gly His Ser Lys Pro Ala Ser Gly His Pro  
 420 425 430  
 Lys Ser Ala Thr Val Tyr Pro Lys Pro Ala Ser Val His Phe Lys Ala  
 435 440 445  
 Asp Ser Val His Phe Lys Gly Asp Ser Val His Phe Lys Pro Asp Ser  
 450 455 460  
 Val His Phe Lys Pro Ala Ser Ser Asn Pro Lys Pro Ile Thr Gly His  
 465 470 475 480  
 His Val Ser Ala Gly Ser His Ser Lys Ser Ala Phe Asn Ala Ala Thr

485

490

495

Ser His Pro Lys Pro Ile Lys Pro Ala Thr Ser His Ala Glu Pro Thr  
                   500                  505                  510

Thr Ala Asp Tyr Pro Lys Pro Ala Thr Thr Ser His Pro Lys Pro Ala  
                   515                  520                  525

Ala Ala Asp Asn Pro Glu Leu Ser Ala Ser His Cys Pro Glu Ile Pro  
                   530                  535                  540

Ala Ile Ala His Pro Val Ser Asp Asp Ser Asp Leu Pro Glu Ser Ala  
                   545                  550                  555                  560

Ser Ser Pro Ala Ala Gly Pro Thr Lys Pro Ala Ala Ser Gln Leu Glu  
                   565                  570                  575

Ser Asp Thr Ile Ala Asp Leu Pro Asp Pro Thr Val Val Thr Thr Ser  
                   580                  585                  590

Thr Asn Asp Tyr His Asp Val Val Val Val Asp Val Glu Asp Asp Pro  
                   595                  600                  605

Asp Glu Met Ala Val  
                   610

<210> 143  
 <211> 33  
 <212> DNA  
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<220>  
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<400> 143  
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<210> 144  
 <211> 31  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Novel Sequence

<400> 144  
 ctccttcggt cctcctatcg ttgtcagaag t

31

<210> 145  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Novel Sequence

<400> 145  
 ttagatatcg gggcccaccc tagcgggt

27

<210> 146  
 <211> 29  
 <212> DNA

<213> Artificial

<220>

<223> Novel Sequence

<400> 146

ggtacccccca cagccatttc atcaggatc

29

ggtacccccca cagccatttc atcaggatc